

FIG.1



GGC ACC GGG GCG CCG CCG CCG CTG CTG CTA CTG CCG CTG CTG CTG CTC CTA GGG ACC GGC
Gly Thr Gly Ala Pro Pro Pro Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Gly Thr Gly

CTC TTG CCT GCT AGC AGC CAC ATA GAG ACC CCG GCC CAT GCG GAG GAG CCG CTC CTG AAG
Leu Leu Pro Ala Ser Ser His Ile Glu Thr Arg Ala His Ala Glu Glu Arg Leu Leu Lys

AGA CTC TTC TCC GGT TAC AAC AAG TGG TCT CCG CCA GTA GGC AAT ATC TCA GAT GTG GTC
Arg Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg Pro Val Gly Asn Ile Ser Asp Val Val

CTC GTC CCG TTT GGC TTG TCC ATT GCT CAG CTC ATT GAC GTG GAC GAG AAG AAC CAG ATG
Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met

ATG ACA ACC AAC GTG TGG GTG AAG CAG GAG TGG CAC GAC TAC AAG CTG CCG TGG GAC CCT
Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp Pro

GGT GAC TAC GAG AAT GTC ACC TCC ATC CCG ATC CCC TCT GAA CTC ATC TGG AGG CCT GAC
Gly Asp Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp

ATC GTC CTC TAC AAC AAT GCG GAT GGA GAC TTT GCA GTC ACC CAC CTG ACC AAG GCC CAC
Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His

CTG TTC TAT GAC GGA AGG GTG CAG TGG ACA CCC CCA GCC ATC TAT AAG AGC TCC TGC AGC
Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser

ATC GAC GTC ACC TTC TTC CCC TTT GAC CAG CAG AAC TGT ACC ATG AAG TTT GGA TCC TGG
Ile Asp Val Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys Phe Gly Ser Trp

ACC TAC GAC AAG GCC AAG ATT GAC TTA GTG AGC ATT CAT AGC CGT GTG GAC CAA CTG GAC
Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Ile His Ser Arg Val Asp Gln Leu Asp

TTC TGG GAA AGT GGG GAG TGG GTC ATC GTG GAT GCT GTG GGC ACC TAC AAC ACC AGG AAG
Phe Trp Glu Ser Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys

TAC GAG TGC TGT GCC GAG ATC TAT CCT GAC ATC ACC TAT GCC TTC ATC ATC CGA CCG CTG
Tyr Glu Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Phe Ile Ile Arg Arg Leu

CCG CTA TTC TAC ACC ATC AAC CTC ATC ATC CCG TGC CTG CTC ATC TCC TGT CTC ACC GTG
Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr Val

FIG. 2A-1



790 810 830
CTG GTC TTC TAT CTG CCT TCA GAG TGT GGC GAG AAG GTC ACA CTG TGC ATC TCG GTG CTG
Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu

850 870 890
CTT TCT CTC ACC GTC TTC CTG CTG CTC ATC ACC GAG ATC ATC CCG TCC ACC TCG CTG GTG
Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val

910 930 950
ATC CCG CTC ATC GGC GAG TAC CTC CTC TTC ACC ATG ATC TTC GTC ACC CTC TCC ATC GTG
Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val

970 990 1010
ATC ACG GTC TTC GTG CTC AAT GTG CAC CAC CCG TCG CCA CGC ACA CAC ACG ATG CCC GGC
Ile Thr Val Phe Val Leu Asn Val His Arg Ser Pro Arg Thr His Thr Met Pro Ala

1030 1050 1070
TGG GTG CGT AGA GTC TTC CTG GAC ATC GTG CCT CGC CTC CTC TTC ATG AAG CGC CCC TCT
Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser

1090 1110 1130
GTG GTC AAA GAC AAC TGC CGG AGA CTT ATT GAG TCC ATG CAC AAG ATG GCC AAC GCC CCC
Val Val Lys Asp Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala Pro

1150 1170 1190
CGC TTC TGG CCA GAG CCT GTG GGC GAG CCC GGC ATC TTG AGT GAC ATC TGC AAC CAA GGT
Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser Asp Ile Cys Asn Gln Gly

1210 1230 1250
CTG TCA CCT GCC CCA ACT TTC TGC AAC CCC ACG GAC ACA GCA GTC GAG ACC CAG CCT ACG
Leu Ser Pro Ala Pro Thr Phe Cys Asn Pro Thr Asp Thr Ala Val Glu Thr Gln Pro Thr

1270 1290 1310
TGC AAG TCA CCC CCC CTT GAG GTC CCT GAC TTG AAG ACA TCA GAG GTT GAG AAG GCC AGT
Cys Arg Ser Pro Pro Leu Glu Val Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala Ser

1330 1350 1370
CCC TGT CCA TCG CCT GGC TCC TGT CCT CCA CCC AAG AGC AGC AGT GGG GCT CCA ATG CTC
Pro Cys Pro Ser Pro Gly Ser Cys Pro Pro Pro Lys Ser Ser Ser Gly Ala Pro Met Leu

1390 1410 1430
ATC AAA GCC AAG TCC CTG AGT GTC CAG CAT GTG CCC AGC TCC CAA GAA GCA GCA GAA GAT
Ile Lys Ala Arg Ser Leu Ser Val Gln His Val Pro Ser Ser Gln Glu Ala Ala Glu Asp

1450 1470 1490
GGC ATC CCG TGC CCG TCT CCG AGT ATC CAG TAC TGT GTT TCC CAA GAT GGA GCT GCC TCC
Gly Ile Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Ser Gln Asp Gly Ala Ala Ser

1510 1530 1550
CTG GCT GAC AGC AAG CCC ACC AGC TCC CCG ACC TCC CTG AAG GCC CGT CCA TCC CAG CTT
Leu Ala Asp Ser Lys Pro Thr Ser Ser Pro Thr Ser Leu Lys Ala Arg Pro Ser Gln Leu

FIG.2A-2



1570 1590 1610
CCC GTG TCA GAC CAG GCC TCT CCA TGC AAA TGC ACA TGC AAG GAA CCA TCT CCT GTG TCC
Pro Val Ser Asp Gln Ala Ser Pro Cys Lys Cys Thr Cys Lys Glu Pro Ser Pro Val Ser

1630 1650 1670
CCA GTC ACT GTG CAC AAG GCG GGA GGC ACC AAA GCA CCT CCC CAA CAC CTG CCC CTG TCA
Pro Val Thr Val Leu Lys Ala Gly Gly Thr Lys Ala Pro Pro Gln His Leu Pro Leu Ser

1690 1710 1730
CCA GCC CTG ACA CGG GCA GTA GAA GGC GTC CAG TAC ATT GCA GAC CAC CTC AAG GCA GAA
Pro Ala Leu Thr Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp His Leu Lys Ala Glu

1750 1770 1790
GAC ACT GAC TTC TCG GTG AAG GAG GAC TGG ACC AAA TAC GTG GCC ATG GTC ATT GAC CGA ATC
Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile

1810 1830 1850
TTC CTC TGG ATG TTC ATC ATT GTC TGC CTT CTG GGC ACT GTG GGA CTC TTC CTG CCT CCC
Phe Leu Trp Met Phe Ile Ile Val Cys Leu Lue Gly Thr Val Gly Leu Phe Leu Pro Pro

1870 1890 1917
TGG CTG GCT GCT TGC TGA TGGCTTCGACAAGTGTCTCAAGGCTCACGTCTCTGCTGACTTTGTTTCCAG
Trp Leu Ala Ala Cys

1943 1969 1997
TTTCTTCTCCGACAAAGTTGGCCTCCCTTCATTTATTCCTGTTATTTTGGGCTTCGTGTTATTAATATCCTTCCCTGCC
TCTGTGGCGCATTGTAAGTTTTAAAAATTAATAGACCAAAGCC...3'

2022 2048
TCTGTGGCGCATTGTAAGTTTTAAAAATTAATAGACCAAAGCC...3'

4-2 cDNA: 3' end

1867 1884 1912
CCC TGG CTG GCT GGT ATG ATC TAG GGACGTGGTGGTGCCAGCTCCACATCTCTGTAGGGCCATAC
Pro Trp Leu Ala Gly Met Ile

1937 1963 1991
GACTCGTCAGTCACCCACATCTTCCAAACCGGCTGACCATGAGACACCCTAGGAGAGAGATGATGCTTCTTGGGAGATG

2016 2042 2070
GAAGTTGGCCCTGGTTCTAGTCAGACTATGGGCGTGGTTGGAGAGAAATGAGGGCTGATACAGTTGCAGGCCGAGTCCC

2095 2121 2149
CATTAAAGTTTCTCCAGAGCAAGTGGCAGTACTCCCTGACTTACAGACAGCACACCCATCTGTGTACAGAGAATGA

2174 2200 2228
TCCCGAGTTGATCTCAGTTGTCTTTGAGGCCATGAAAAATTCATCCACCTTGAGGAACAGAGCCTCTCATGCTGTGG

2253 2279 2307
GATCAATAAGACAGGAATCTCCCACTGTGACTCTGCTGGCCACACCCTCTCCCTCCCAAGAAGTGGTCCCTCATCC
CCCAATTC...3'

FIG.2A-3

ATAAAGTCTCCGGCAGTTGTCTTTGACCACAGAGGGACGAGCGCGCGCGATGAACTTGGGTGGCGCGCAGCTCTGGAGCGGAGGGCGGGCACAGCGGGCGAGCCGCCGCA
-210 -180 -150 -120

[illegible]

FIG. 2B-1

Asp	Phe	Trp	Glu	Ser	180	Glu	Trp	Val	Ile	Val	Ile	Asp	Ala	Val	Gly	Thr	Asn	Thr	Arg	Lys	Tyr	Glu	Cys	200	Glu	Ile	Tyr	Pro
GAC	TTC	TGG	GAA	AGT	540	GAG	TGG	GTC	ATC	GTG	GAT	GCT	GTG	GGC	ACC	TAC	AAC	ACC	AGG	AAG	TAC	GAG	TGT	600	GAG	ATC	TAT	CCT
Asp	Ile	Thr	Tyr	Ala	210	Ile	Ile	Arg	Arg	Leu	Pro	Leu	Phe	Thr	Tyr	Ile	Asn	Leu	Ile	Pro	Cys	Leu	230	Ser	Cys	Leu	Thr	
GAC	ATC	ACC	TAT	GCC	630	ATC	ATC	CGA	CGC	CTG	CCG	CTA	TTC	TAC	ACC	ATC	AAC	CTC	ATC	CCG	TGC	CTG	690	ATC	TCC	TGT	CTC	
Val	Leu	Val	Phe	Tyr	240	Pro	Ser	Glu	Cys	Gly	Gly	Lys	Val	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu	Ser	260	Phe	Leu	Leu	Leu	
GTG	CTG	GTC	TAT	TTC	720	CTT	TCA	GAG	TGT	GGC	GAG	AAG	GTC	ACA	CTG	TGC	ATC	TCC	GTC	CTT	TCT	CTC	780	TTC	CTG	CTG	CTC	
Ile	Thr	Glu	Ile	Ile	270	Ser	Thr	Ser	Leu	Val	Ile	Pro	Leu	Ile	Gly	Gly	Tyr	Leu	Leu	Phe	Thr	Met	290	Thr	Leu	Ser	Ile	
ATC	ACC	GAG	ATC	ATC	810	TCC	ACC	TCC	CTG	ATC	ATC	CCG	CTC	ATC	GGC	GAG	TAC	CTC	CTC	TTC	ACC	ATG	870	ACC	CTC	TCC	ATC	
Val	Ile	Thr	Val	Phe	300	Leu	Asn	Val	Ile	His	His	Arg	Ser	Pro	Arg	Thr	His	Thr	Met	Pro	Ala	Irp	320	Phe	Leu	Asp	Ile	
GTG	ATC	ACG	GTC	TTC	900	CTC	AAT	GTG	CAC	CAC	CAC	CGC	TGC	CCA	CGC	ACA	CAC	ACG	ATG	CCC	GCC	TGG	360	TTC	CTG	GAC	ATC	
Val	Pro	Arg	Leu	Leu	330	Met	Lys	Arg	Pro	Ser	Val	Val	GTC	AAA	GAC	Asn	Cys	Arg	Arg	Leu	Ile	Glu	350	Met	Ala	Asn	Ala	
GTG	CCT	CGC	CTC	CTC	990	ATC	ATG	AAG	CGC	CCC	TCT	GTG	ATC	AAA	GAC	AAC	TGC	CGG	AGA	CTT	ATT	GAG	1050	ATG	GCC	AAC	GCC	
Pro	Arg	Phe	Trp	Pro	360	Pro	Val	Gly	Glu	Pro	Gly	Ile	Leu	Ser	Asp	Ile	Cys	Asn	Gln	Gly	Leu	Ser	380	Thr	Phe	Cys	Asn	
CCC	CGC	TTC	TGG	CCA	1080	CGT	GTG	GGC	GAG	CCC	GGC	ATC	TTG	AGT	AGT	ATC	TGC	AAC	CAA	GGT	CTG	TCA	410	ACT	TTC	TGC	AAC	
Pro	Thr	Asp	Thr	Ala	390	Glu	Thr	Gln	Pro	Thr	Cys	Arg	Ser	Pro	Pro	Leu	Glu	Val	Pro	Asp	Leu	Lys	430	Val	Glu	Lys	Ala	
CCC	ACG	GAC	ACA	GCA	1170	GTG	GAG	ACC	CAG	CCG	TGC	AGG	TCA	CCC	CCC	CTT	GAG	GTC	CCT	GAC	TTG	AAG	1230	GTT	GAG	AAG	GCC	

FIG. 2B-2



Ser Pro Cys Pro Ser 420 Gly Ser Cys Pro Pro Lys Ser Ser 430 Gly Ala Pro Met Leu Ile Lys Ala Arg Ser 440 Leu Ser Val Gln
AGT CCC TGT CCA TGG CCT GGC TCC TCT CCA CCC CCA AAG AGC AGC 1260 TCC CCA AAG GGC AGG 1320 TCC CAA GAT GCT GGC
His Val Pro Ser Ser 450 Glu Ala Ala Glu Asp Gly Ile Arg Cys Arg 460 Ser Arg Ser Ile Gln Tyr Cys Val Ser Gln Asp Gly Ala Ala
CAT GTG CCC AGC TCC CAA GAA GCA GCA GAA GAT GGC ATC GGC TCC CCA GAT TCC CAA GAT GGC 1410 TCC CAA GAT GGC
Ser Leu Ala Asp Ser Lys 480 Pro Thr Ser Ser Pro Thr Ser Leu Lys Ala Arg Pro Ser Gln Leu Pro Val Ser Asp Gln Ala Ser Pro Cys
TCC CTG GCT GAC AGC CCC ACC ACC TCC TCC CCG ACC TCC CCA GTC ACT GTG CTC AAG GGC 1470 CCA GAT TCA GAC CAG GCC TCT CCA TGC
Lys Cys Thr Cys Lys 510 Pro Ser Pro Val Ser Pro Val Thr Val Leu Lys Ala Gly Gly Thr Lys Ala Ala Pro Pro Gln His Leu Pro Leu
AAA TGC ACA TGC AAG GAA CCA TCT CCT GTG TCC CCA GTC ACT GTG CTC ACT GTG CTC AAG GCG GGA GGC ACC AAA GCA CCT CCC CAA CAC CTG CCC CTG
Ser Pro Ala Leu Thr Arg 540 Ala Val Glu Gly Val Gln Tyr Ile Ala Asp His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu Asp
TCA CCA GCC CTG ACA CGG GCA GTA GTC GTC CAG TAC TAC ATT GCA GAC CAC CTC AAG GCA GAA GAA GAC ACT GAC TTC TCG GTG AAG GAG GAC 1680
Trp Lys Tyr Val Ala Met 570 Val Ile Asp Arg Ile Phe Leu Trp Met 580 Phe Ile Ile Val Cys Leu Leu Gly Thr Val Val Gly Leu Phe Leu Pro
TGG AAA TAC GTG GGC ATG ATG GTC ATT GAC CGA ATC TTC CTC TGG TGG ATG TTC TCC TCC CCA GTC ACT GTG GGC ACT GTG GGC 1770
Pro Trp Leu Ala Gly Met 600 * Ile
CCC TGG CTG GCT GGT ATG ATC TAG GGACGTGGTGGTGCCAGCTCCACATCTCTGTAGGGCCATACGACTCGTCAGTCCACCCACATCTTCCAAACCGGCTGACCATGAG 1890
ACACCTAGGAGAGAGATGCTTCTTGGGAGATGGAAATTGGCCCTGGTTCTAGTCAGACTATGGGCGTGGTTGGAGAGAAATGAGGGCTGATACAGTTGCAGGCCGAGTCCCCATT 2010
1920 1950 1980 1990

FIG.2B-3

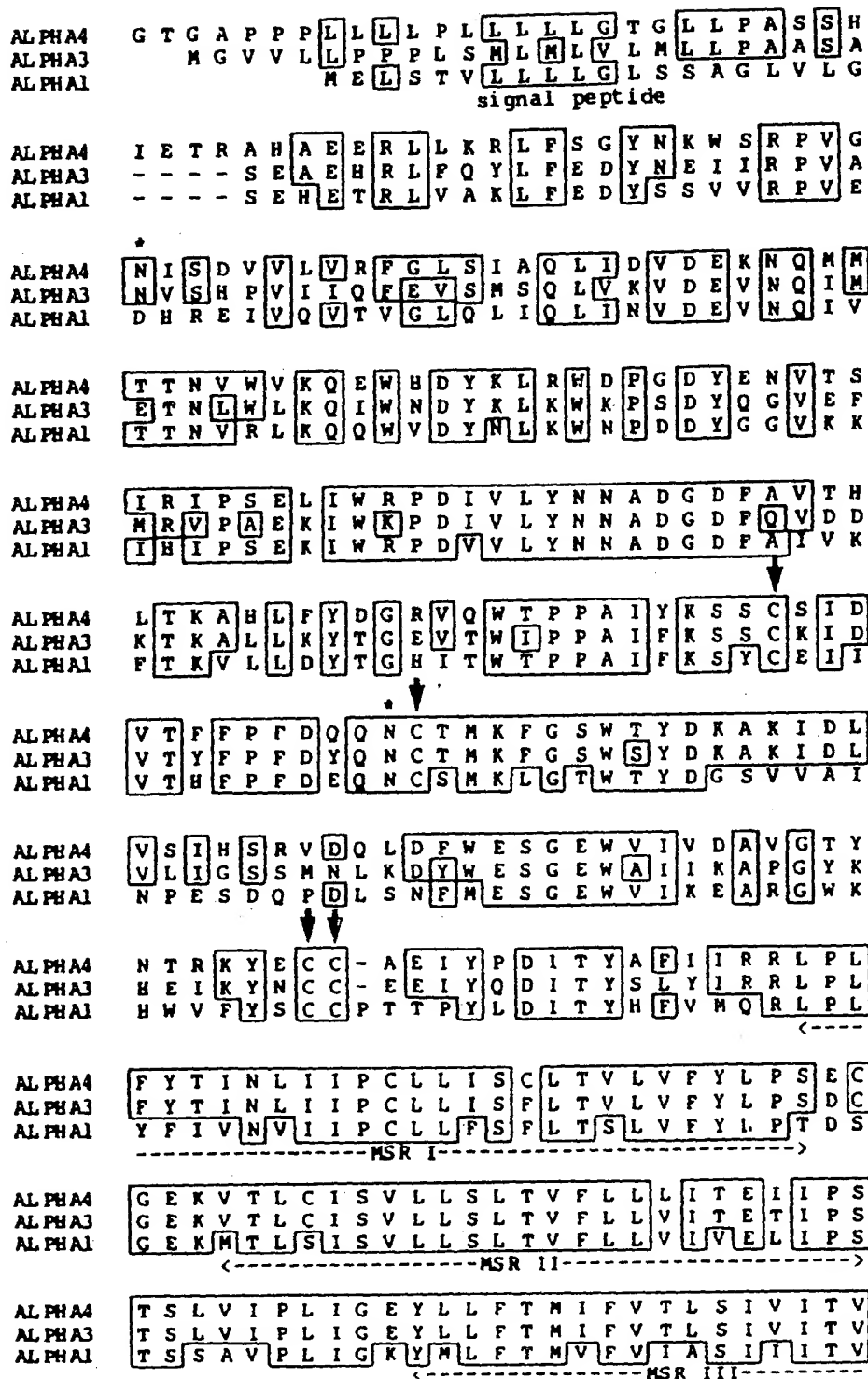


FIG.3A



ALPHA4 F V L N V H H R S P R T H T M P A W V R R V F L D I V
ALPHA3 F V L N V H Y R T P T T H T M P T W V K A V F L N L L
ALPHA1 I V I N T H H R S P S T H I M P E W V R K V F I D T I
----->

ALPHA4 P R L L F - - - M K R P S V V K D N C R R L I E S M H
ALPHA3 P R V M F - - - M T R P T S G E G D T P K T - - - -
ALPHA1 P N I M F F S T M K R P S R D K Q E K R I F - - - -

ALPHA4 K M A N A P R F W P E P V G E P G I L S D I C N Q G L
ALPHA3 - - - - - - - - - - R T F Y G A E L S N L N C F S R
ALPHA1 - - - - - - - - - - T E D I D I S D I S G K P G

ALPHA4 S P A P T F C N P T D T A V E T Q P T C R S P P L E V
ALPHA3 A D S K S C K E G Y P C Q D G T C G Y C H H R R V K I
ALPHA1 P P P M G F H - - - - - - - - - - - - - - - - - -

ALPHA4 P D L K T S E V E K A S P C P S P G S C P P P K S S S
ALPHA3 S N F - - - - - - - - - - - - - - - - - - S A N L T R S S S
ALPHA1 -

ALPHA4 G A P M L I K A R S L S V Q H V P S S Q E A A E D G I
ALPHA3 S E S V - - - - - - - - - - - - - - - - - -
ALPHA1 -

ALPHA4 R C R S R S I Q Y C V S Q D G A A S L A D S K P T S S
ALPHA3 -
ALPHA1 -

ALPHA4 P T S L K A R P S Q L P V S D Q A S P C K C T C K E P
ALPHA3 -
ALPHA1 -

ALPHA4 S P V S P V T V L K A G G T K A P P Q H L P L S P A L
ALPHA3 - - - - - - - - - - - - - - - - - - N A V L S L S A L S P E I
ALPHA1 - - - - - - - - - - - - - - - - - - S P L I K H P E V
-----<

ALPHA4 T R A V E G V Q Y I A D H L K A E D T D F S V K E D W
ALPHA3 K E A I Q S V K Y I A E N M K A Q N V A K E I Q D D W
ALPHA1 K S A I E G V K Y I A E T M K S D Q E S N N A A E E W
amphipathic helix----->

ALPHA4 K Y V A M V I D R I F L W M F I I V C L L G T V G L F
ALPHA3 K Y V A M V I D R I F L W V F I L V C I L G T A G L F
ALPHA1 K Y V A M V M D H I L L G V F H L V C L I G T L A V F
-----<-----MSR IV----->

ALPHA4 L P P W L A G M I
ALPHA3 L Q P L M A - R D D T
ALPHA1 A G R L I E L H Q Q G
----->

FIG.3B

FIG.4A

Clone 4-1;
Antisense

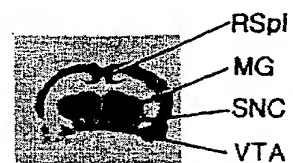
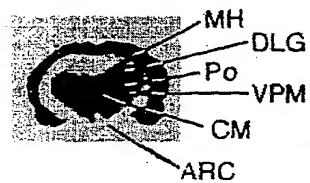
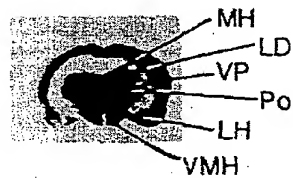
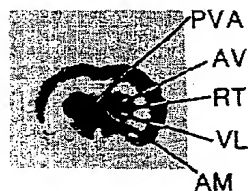


FIG.4B

Clone 4-1;
Sense

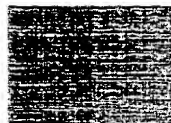
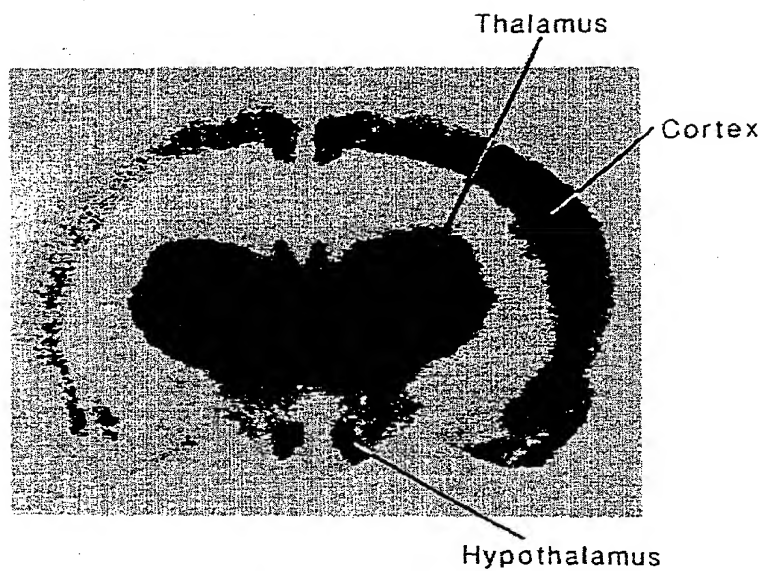


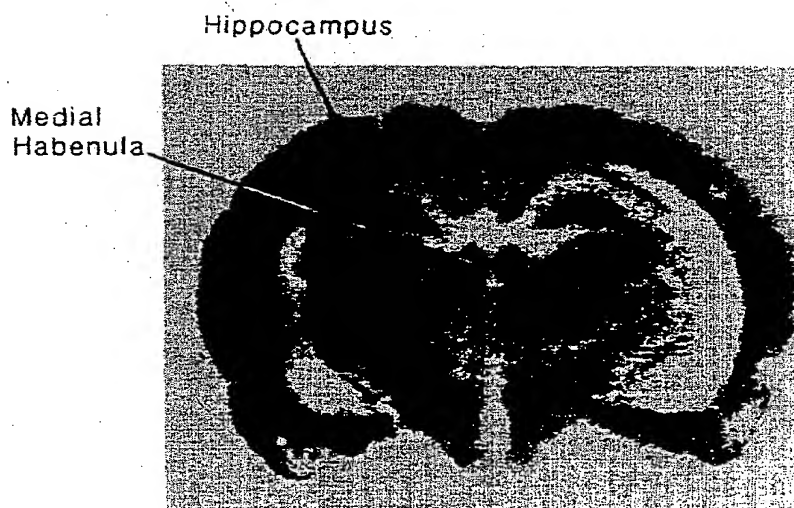


FIG.5A



PROBE: Alpha 4

FIG.5B



PROBE: Alpha 3

FIG.6A

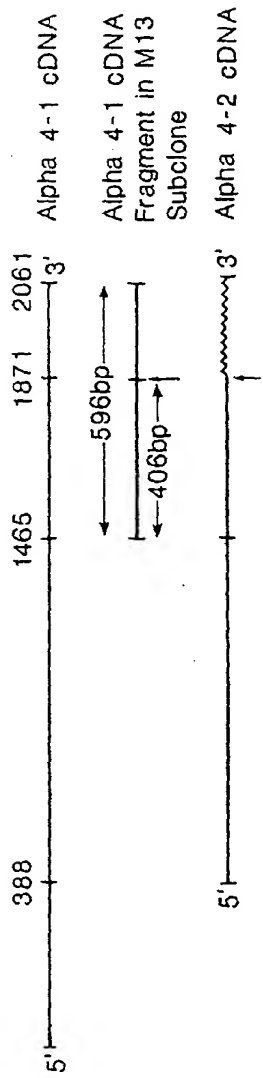


FIG.6B

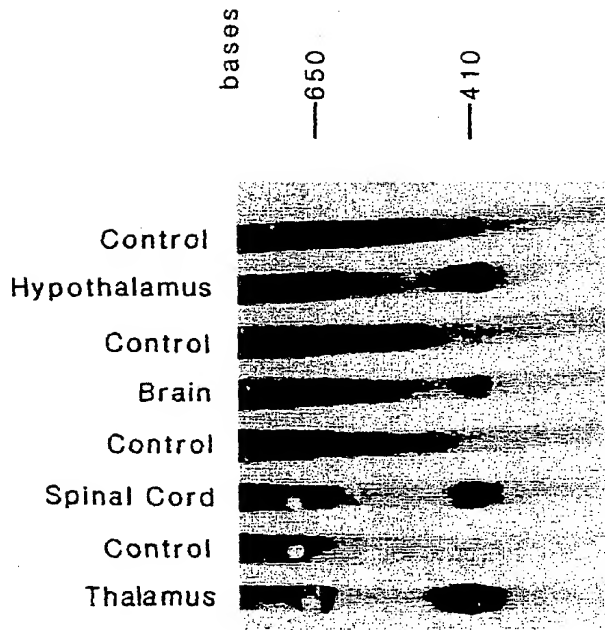
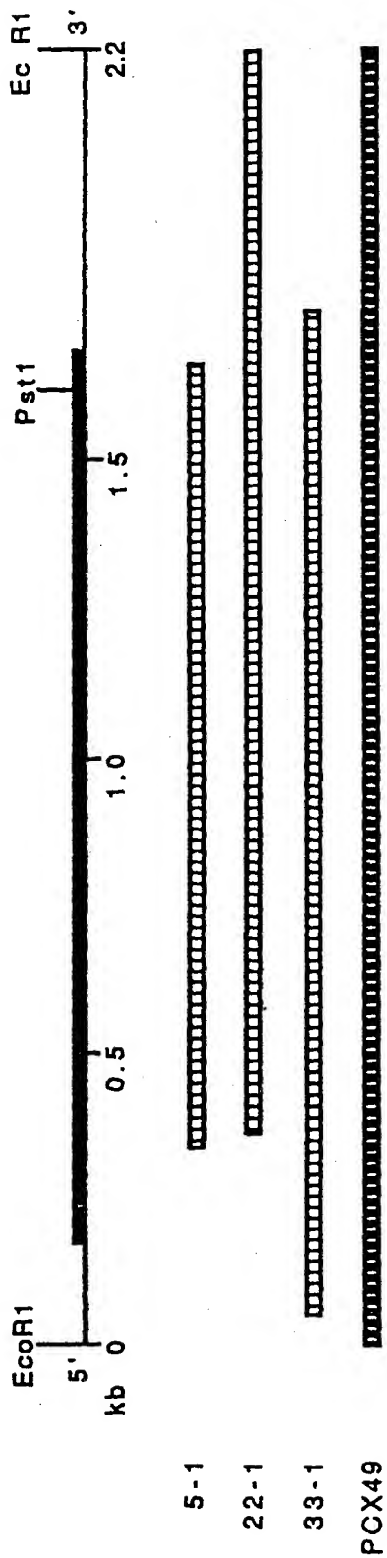




FIG.7A





5' -179 -100
GGGAAACACAACCGGGACCGGCAAGAAGCCGGGACCTCCCTCGTTGCAGGAACCTGCCCGTTTCAGTGAGCACTTTAGACC
TGGAGGCCGGAGCCCGGACCCCGGAGCAGGGGGCTGGCGGGCTTCAGCACCCAGGAGCGCTCGACCCCGCAGCCCTAGTATCCGAGAGGCTGCGCGCT
ATG CTG GCT TGC ATG GCC GGG CAC TCC AAC TCA ATG GCG CTG TTC AGC TTC AGC CTT CTT TGG CTG TGC TCA GGG
Met Leu Ala Cys Met Ala Gly His Ser Asn Ser Met Ala Leu Phe Ser Phe Ser Leu Leu Trp Leu Cys Ser Gly
1 60
GTT TTG GGA ACT GAC ACA GAG GAG CGG CTA GTG GAG CAT CTC TTA GAT CCC TCC CGC TAT AAC AAG CTG ATT CGT
Val Leu Gly Thr Asp Thr Glu Glu Arg Leu Val Glu His Leu Leu Asp Pro Ser Arg Tyr Asn Lys Leu Ile Arg
26 90
CCA GCT ACT AAC GGC TCT GAG CTG GTG ACT GTA CAG CTC ATG GTA TCA TTG GCT CAG CTC ATT AGT GTG CAC GAG
Pro Ala Thr Asn Gly Ser Glu Leu Val Thr Val Glu Leu Met Val Ser Leu Ala Gln Leu Ile Ser Val His Glu
51 180
CGG GAG CAG ATC ATG ACC ACC AAT GTC TGG CTG ACC CAG GAG TGG GAA GAT TAC CGC CTC ACA TGG AAG CCT GAG
Arg Glu Gln Ile Met Thr Thr Asn Val Trp Leu Thr Gln Glu Trp Glu Asp Tyr Arg Leu Thr Trp Lys Pro Glu
76 240
GAC TTC GAC AAT ATG AAG AAA GTC CGG CTC CCT TCC AAA CAC ATC TGG CTC CCA GAT GTG GTT CTA TAC AAC AAT
Asp Phe Asp Asn Met Lys Lys Val Arg Leu Pro Ser Lys His Ile Trp Leu Pro Asp Val Val Leu Tyr Asn Asn
101 330
GCT GAC GGC ATG TAC GAA GTC TCC TTC TAT TCC AAT GCT GTG GTC TCC TAT GAT GGC AGC ATC TTT TGG CTA CCA
Ala Asp Gly Met Tyr Glu Val Ser Phe Tyr Ser Asn Ala Val Val Ser Tyr Asp Gly Ser Ile Phe Trp Leu Pro
126 390 420
CCT GCC ATC TAC AAG AGT GCA TGC AAG ATT GAG GTG AAG CAC TTC CCA TTT GAC CAG AAT TGC ACC ATG AAG
Pro Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys
151 480 510

FIG.7B-1



540
 TTT CGC TCA TGG ACC TAC GAC CGT ACT GAG ATT GAC CTG GTG CTC AAA AGT GAT GTG GCC AGT CTG GAT GAC TTC
 Phe Arg Ser Trp Thr Thr Asp Tyr Asp Arg Thr Glu Thr Glu Ile Asp Leu Val Val Leu Lys Ser Asp Val Ala Ser Leu Asp Asp Phe
 176

630
 ACA CCC AGC GGG GAG TGG GAC ATC ATC GCA CTG CCA GGC CGA CGC AAC GAG AAC CCA GAC GAC TCC ACC TAT GTG
 Thr Pro Ser Gly Glu Glu Trp Asp Ile Ile Ala Leu Pro Gly Arg Arg Arg Asn Glu Asn Pro Asp Asp Ser Thr Tyr Val
 201

690
 GAC ATC ACC TAT GAC TTC ATC ATT CGT CGC AAA CCA CTC TTC TAC ACT ATC AAC CTC ATC CCC TGC GTA CTC
 Asp Ile Thr Tyr Asp Phe Ile Ile Arg Arg Arg Tyr Phe Phe Thr Ile Asn Leu Ile Ile Pro Cys Val Leu
 226

780
 ATC ACC TCG CTG GCC ATC CTG GTC TTC TAC TGT GGT GAA AAG ATG ACA CTT TGT ATT TCT GTG
 Ile Thr Ser Leu Ala Ile Leu Val Phe Tyr Tyr Cys Asp Gln Lys Met Thr Thr Cys Ile Ser Val
 251

840
 CTG CTA GCA CTC ACG GTG TTC CTG CTC ATC TCC AAG ATT GTG CCT CCC ACC TCC CTC GAT GTA CCG CTG GTG
 Leu Leu Ala Leu Thr Thr Val Phe Leu Leu Leu Ile Val Val Pro Thr Ser Leu Asp Val Pro Leu Val
 276

930
 GGC AAG TAC CTC ATG TTT ACC ATG GTG CTA GTC ACC TTC TCC ATC ATC AGC GTG TGT GTG CTC AAT GTG CAC
 Gly Lys Tyr Leu Met Phe Thr Met Val Leu Leu Val Thr Phe Ser Ile Val Thr Ser Val Cys Val Leu Asn Val His
 301

990
 CAC CGC TCG CCT ACC ACG CAC ACC ATG GCC CCC TGG GTC AAG GTG GTC TTC CTG GAG AAG CTG CCC ACC CTG CTC
 His Arg Ser Pro Thr Thr His Thr Met Ala Pro Trp Val Lys Val Val Phe Leu Glu Lys Leu Pro Thr Thr Leu Leu
 326

1080
 TTC CTG CAG CAG CCA CGC CAC CGC TGT GCA CGT CAG CGT CTG CGC TTG AGG AGG CGC CAG CGA GAG CGT GAG GGC
 Phe Leu Gln Gln Pro Arg Arg His Arg Cys Ala Arg Gln Arg Leu Arg Arg Arg Gln Arg Glu Arg Glu Gly
 351

570
 720
 810
 870
 960
 1020
 1110

FIG.7B-2



1140
GAG GCG GTT TTC TTC CGT GAA GGT CCT GCG GCT GAC CCA TGT ACC TGC TTT GTC AAC CCT GCA TCA GTG CAG GGC 1200
Glu Ala Val Phe Phe Phe Arg Glu Gly Pro Ala Ala Asp Pro Cys Thr Cys Phe Val Asn Pro Ala Ser Val Gln Gly
376

1230
TTG GCT GGG GCT TTC CGA GCT GAG CCC ACT GCA GCC GGC CCG GGG CGC TCT GTG GGG CCA TGC AGC TGT GGC CTC 1260
Leu Ala Gly Ala Phe Arg Ala Glu Pro Thr Ala Ala Glu Pro Gly Arg Ser Val Gly Pro Cys Ser Cys Gly Leu
401

1290
CAG GAA GCA GTG GAT GGC GTA C6C TTC ATT GCG GAC CAC ATG CGA AGT GAG GAT GAT GAC CAG AGT GTG AGG GAG 1350
Arg Glu Ala Val Asp Gly Val Arg Phe Ile Ala Asp His Met Arg Ser Glu Asp Asp Asp Gln Ser Val Arg Glu
426

1380
GAC TGG AAA TAC GTT GCC ATG GTG ATC GAC CGC CTG TTC CTG TGG ATC TTT GTC TTT GTC TGT GTC TTT GGG ACC 1410
Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Leu Phe Phe Val Phe Val Phe Val Cys Val Phe Gly Thr
451

1440
GTC GGC ATG TTC CTG CAG CCT CTC TTC CAG AAC TAC ACT GCC ACT ACC TTC CTC CAC CCT GAC CAC TCA GCT CCC 1500
Val Gly Met Phe Leu Gln Pro Leu Phe Gln Asn Tyr Thr Ala Thr Thr Phe Leu His Pro Asp His Ser Ala Pro
476

1596
AGC TCC AAG TGAGGTCCTCATTTCAGCTCCTCACCCCGTGACCCCTGCGGTTTCAGTACTGGGTGCAAGATGGATCTCTCCCCACTCCACTGA 1596
Ser Ser Lys

1695
AGCCTGCTTCACACCTCCGTTACACATAGTCCTCCAGCCTGGAGGCTGGACCCCGCTGCCCTTGTTGTCGAGCCTTCTCCTTTCCCTCTGAGCTCGTTCA 1695
GGCAGGAGTGCCCAATGGTGGGGCCACGGCTGGTAAGTAGAGGCCAGAGATCACAGAGCCACCTACCCCGATGAGGTGCTGGAGAGGCGGCCAAGAAAG 1794
AGACAGAGTTATCTGTGACCTCCAAGTCATCGGAGAGGAGGAGGTAGGATAAGGGGCTCAGACTCTGGCAGAGTGC6GCTAGTACTTGGCGCCCAACCA 1893
CTTAAGTGAGCGACACTGGTCTGGGAGGACTCGAAGTGTGGGGAGCTCTCTTTGGGAGCTCGGTCTCCCCACCCCTGTACCTCAGAGGGGCTCCAGACCCCGG 1992
2017
GCTTCAGGTTCCCTTCTGCCAGTGC.....3'

FIG.7B-3

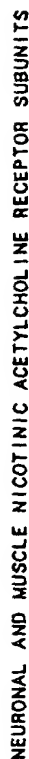


Fig. 8



FIG.9A

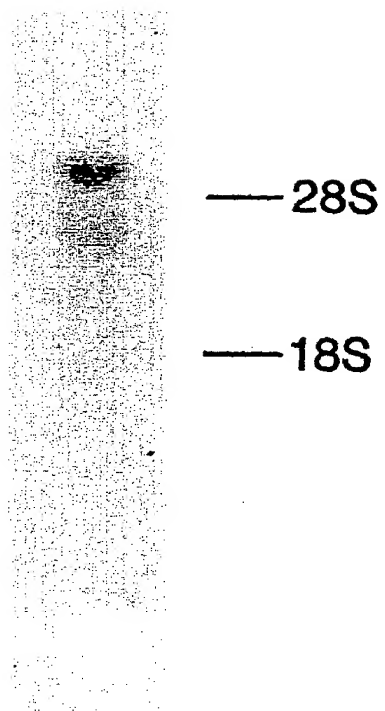


FIG.9B

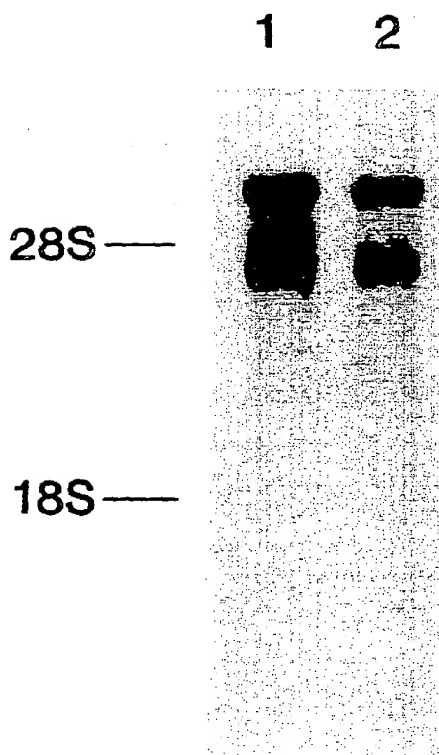




FIG. 10A
ANTISENSE

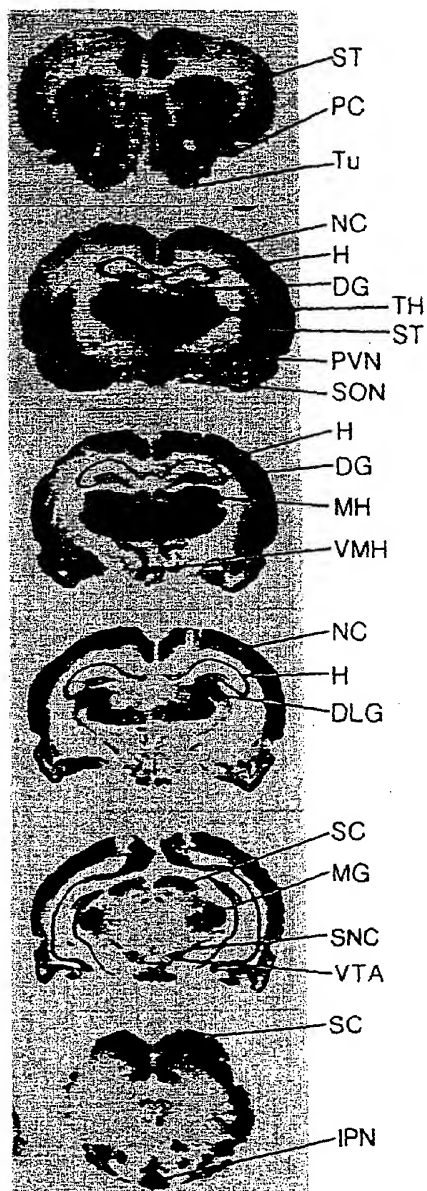


FIG. 10B
SENSE





ALPHA-SUBUNIT COMPARISON

ALPHA 1 MELSTVLLGLSSAGLVGSEHTRNAKLEDESSVVRHVEDHREIPQVTVGLQLIPDIKADIVQDIIVTIVRLKQDQVVDNCKNNDIGGGCKIHIPS
ALPHA 3 MGVVLLPPLSLMLVLMKLLPAASAEAHUIFOYIEDNEIIRPVANVSHPEIQFEVSMGQKVKQDFVQDINEQLWLKGIAMQXKXKXSDVQGGFEFMRVDA
ALPHA 4 MANGSGAPPPLLLPLLLLTGQLPASPASHIETRAKAEMLKRESGKRWSSUNGNISDVLYRFGLSIAQIIOQDIKQZNMNTVWVVKDEMDYKTRADQCDTENVTISIRIQS
SIGNAL PEPTIDE

ALPHA 1 EKTRPDVITDRAUGDAIVKFKVVLQDTTHITTPPAIFKSYCEIETNPTEDEHQSMALEMTTQGSVVAINPESDOPDLSNFHESGEMKERRGNKHWVFISGPTTPPL
ALPHA 3 EKTRPDVITDRAUGDAIVKFKVVLQDTTHITTPPAIFKSYCEIETNPTEDEHQSMALEMTTQGSVVAINPESDOPDLSNFHESGEMKERRGNKHWVFISGPTTPPL
ALPHA 4 ELIMRQIVLTDRAGDAAVTHLEKAEHFDORVQTPPAIFKSYCSIDVETPPIQDZNGTKKFSMTDQKAKIDLVS IHSRVQDQDFVSGEIVVVDVAVGTYNTRKEGGAELIP
ACETYLCHOLINE

ALPHA 1 DITTHFYMQRPPIVFIQVTPGCLTFHETSEVHTITQSMKMTISGVLLSIVALLVMTLPSTSSAVPLIGKAGCTMVVIAQIITVIMVITTHISSTHIMHIEWVRKVF
ALPHA 3 DITTHFYMQRPPIVFIQVTPGCLTFHETSEVHTITQSMKMTISGVLLSIVALLVMTLPSTSSAVPLIGKAGCTMVVIAQIITVIMVITTHISSTHIMHIEWVRKVF
ALPHA 4 DITTHFYMQRPPIVFIQVTPGCLTFHETSEVHTITQSMKMTISGVLLSIVALLVMTLPSTSSAVPLIGKAGCTMVVIAQIITVIMVITTHISSTHIMHIEWVRKVF
MEMBRANE SPANNING I

ALPHA 1 IDTIDHIMFESTMKRPSBOKKRIPTEDIDISDLSCKGPPMGFFH
ALPHA 3 LNLIRVMTATRPISGEGDTPKTRTFYGAELSNLACFSRADSKCKEGYPCODGTGCGYCHRRRVKISNFSANLTRSSSESSEVNAV
ALPHA 4 LDIVHLLAKRPSVVKONCRRLIESHKMANAPRFWPEVGPGLSDICHQGLSPAPTFCNPTDQAVETOPTCRSPPLEVPDLKTSEVEKASPCPSGSCPPPKSSSGAPMLIXA
CYTOPLASMIC REGION

ALPHA 1 RSLSVQHVPSSQEAEDGIACRSRSIQYCVSQDGGAAADSKPTSSPTSLKARPSOLPVSDQASPCCKCTCKEPPSPVTVLKAGGTKAPPOHLPLSLALTRVEGQIADHLAE
ALPHA 3 RSLSVQHVPSSQEAEDGIACRSRSIQYCVSQDGGAAADSKPTSSPTSLKARPSOLPVSDQASPCCKCTCKEPPSPVTVLKAGGTKAPPOHLPLSLALTRVEGQIADHLAE
ALPHA 4 RSLSVQHVPSSQEAEDGIACRSRSIQYCVSQDGGAAADSKPTSSPTSLKARPSOLPVSDQASPCCKCTCKEPPSPVTVLKAGGTKAPPOHLPLSLALTRVEGQIADHLAE
AMPHIPATHIC HELIX

ALPHA 1 QESNNAAEENSTSDVILGVNMLLILFLAVAGRLIELHQOG
ALPHA 3 NVAKEIGDDVSTSDVILGVNMLLILFLAVAGRLIELHQOG
ALPHA 4 DTQFSVKEDVSTSDVILGVNMLLILFLAVAGRLIELHQOG
MEMBRANE SPANNING IV

FIG.11

Responses to
Nicotine (Nic)

Responses to
Acetylcholine (ACh)

mRNAs
injected

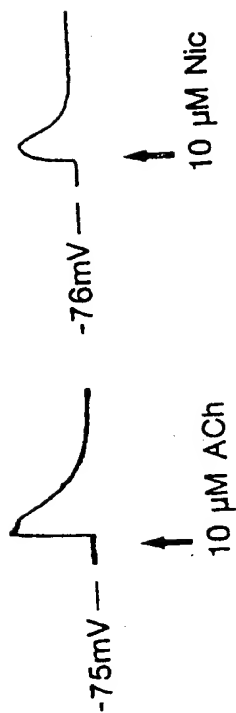


FIG.13A alpha3
+ beta2

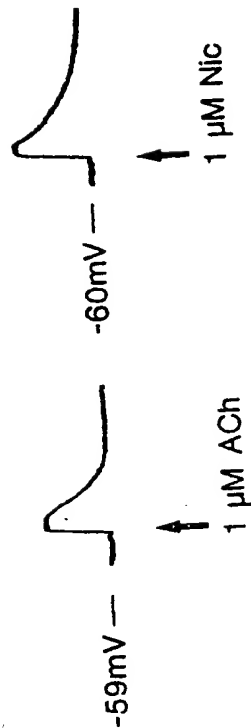


FIG.13B alpha4
+ beta2

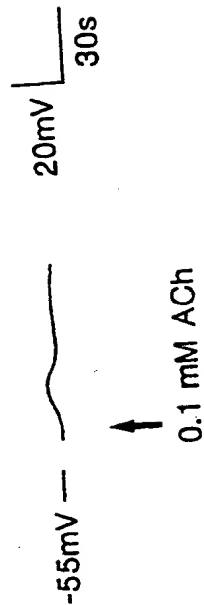
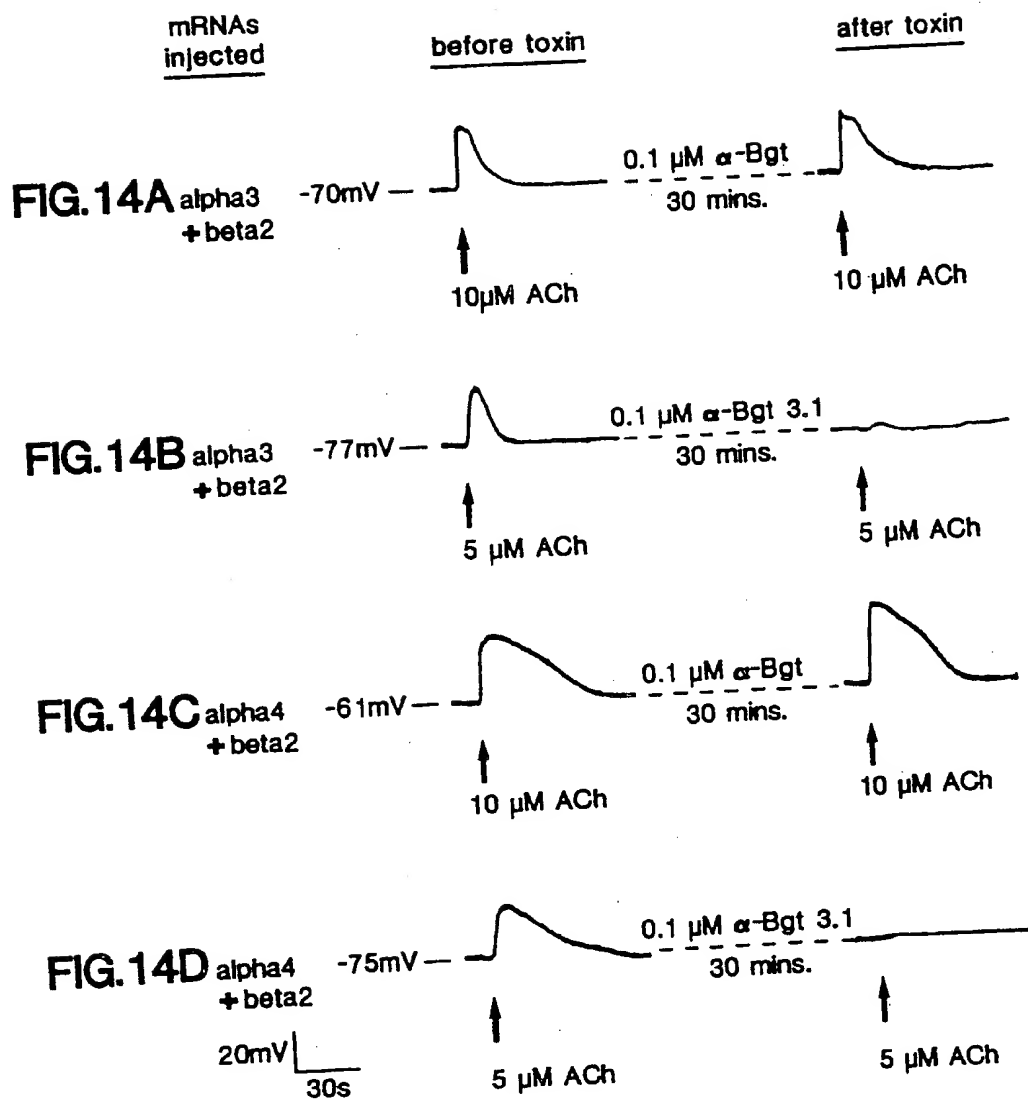


FIG.13C alpha4



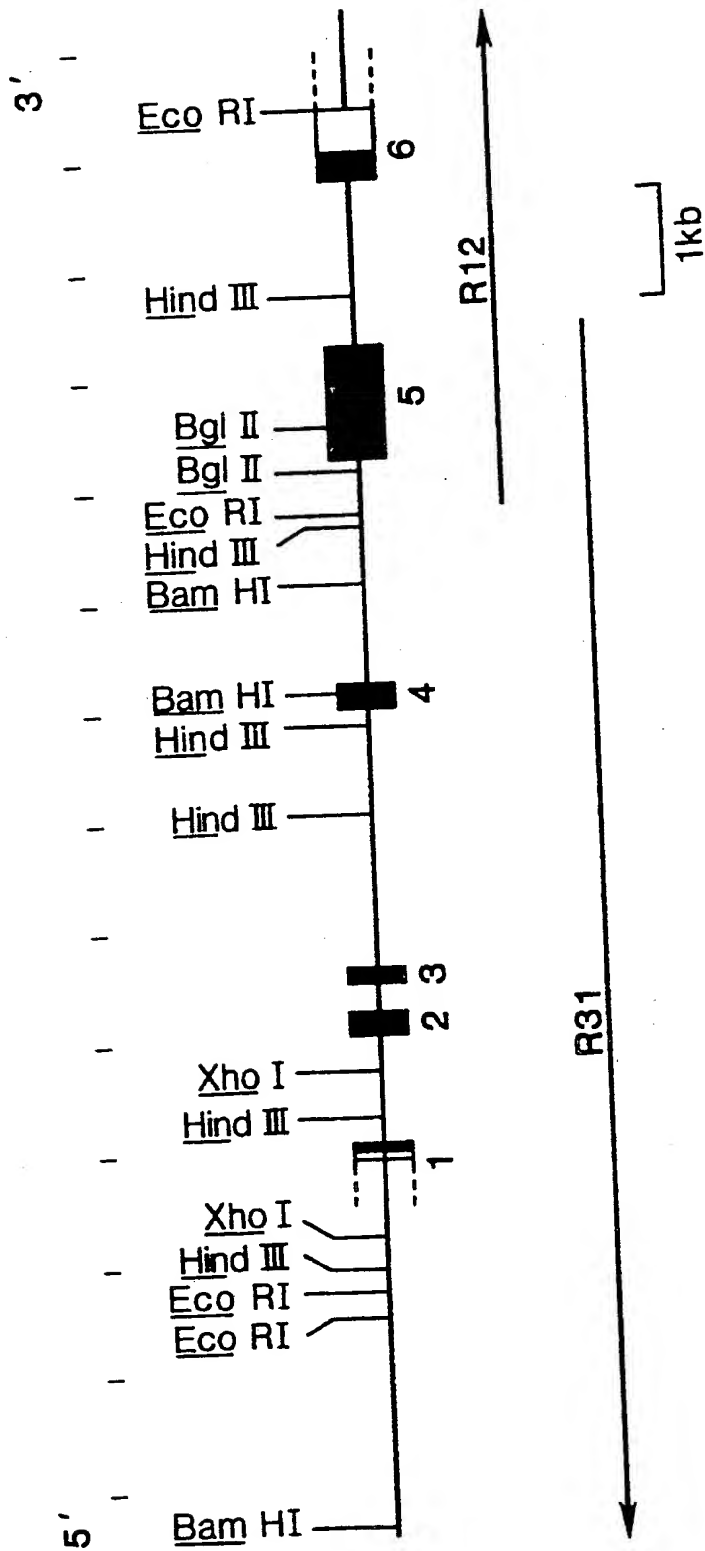


FIG.15A

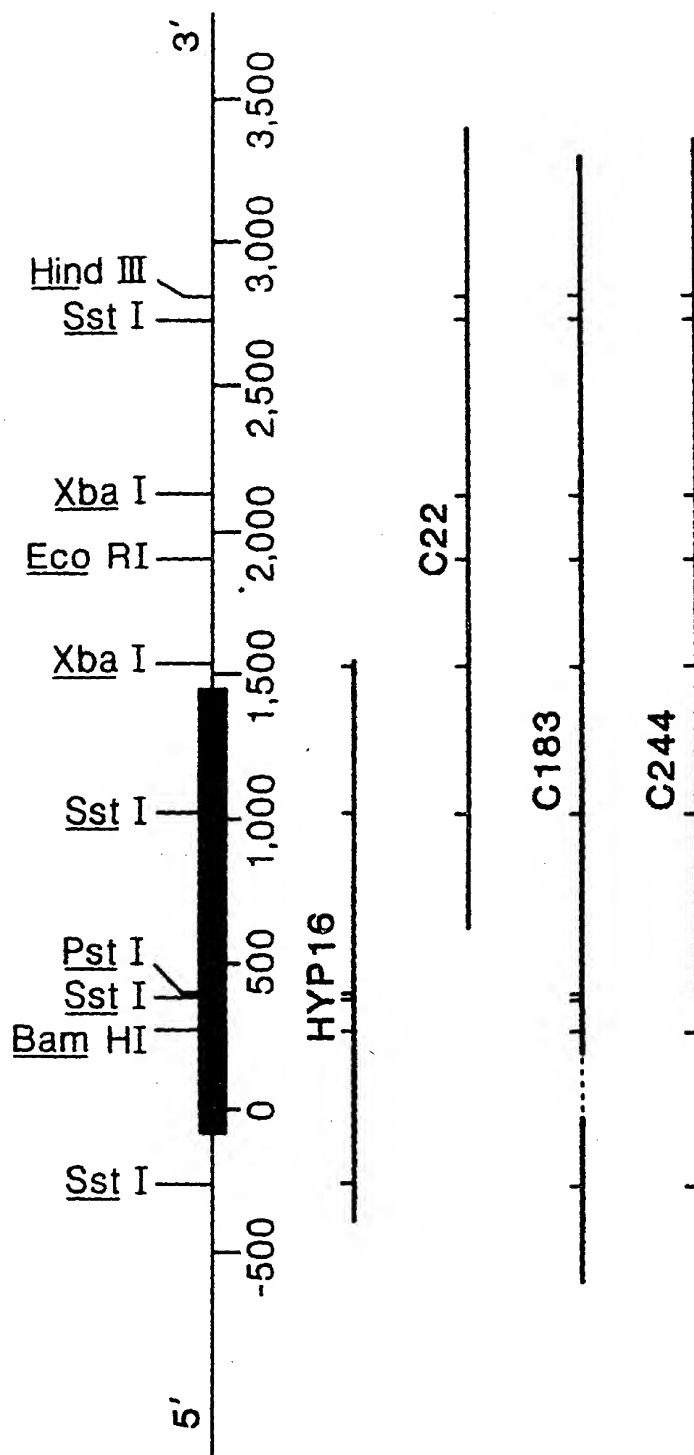


FIG. 15B



5'.....ACTGAGCATTC
-360 TGTGAACTCGGATCACCTATCTCCAGGAAGCTAGCCTGAATCCCTCATCCCAACAGTGCCTCCCAACCTTGACGGTTCTGTGTCTGGGCAACCATGAGCTGAAGCAACTGAGCTCTG
-330
-270
-240 TTCTGCACCTGTCTACTGCTCCGAGGGACCTCGTCAAGCCACCCCGGTCTCCAGCCGGTTGGTTCTCTGCAATCCCTTGAGGGGCTGTCTTCTCTATGACAATTGCAGAGAGACAGT
-210
-180
-150
-120 GCCTCAAGAAGCCAGCTCTTGGTAGTCCAAAGGGAACCAAGGACCTCTCTGAAGCC ATG ACC CTT TCC CAT TCT GCT CTC CAG TTC TGG ACA CAT CTT TAT CTC
-90
-60
-30 TGG TGT CTC CTT CTG GTG CCA GCA G gtgagt.....tatccacag TG TTG ACC CAG CAA GGC TCA CAC ACC CAT GCT GAG GAC CGC CTG TTC
Trp Cys Leu Leu Val Pro Ala V al Leu Thr Gln Gln Gly Ser His Thr His Ala Glu Asp Arg Leu Phe
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270 ATC TGG ATC CCA GAC ATT GTC CTC TAC AAC AA gtaaga.....ctcttcccag T 330 ACC AAG
ile Trp ile Pro Asp ile Val Leu Tyr Asn As 100 n 110 Met Thr Lys
90
360 GCT CAC CTC TTC TTC ACG GGC Thr Gly 120 420 TTC CCC TTC
Ala His Leu Phe Phe Thr Gly 130 Ser Ser Cys Ser ile Asp Val Thr Phe 140 Phe Pro Phe
450 GAC CAG CAG AAC TGC AAG ATG AAG 480 ATC GAT CTG GAG CAG ATG GAG AGG ACA 510 GAC CTG
Asp Gln Gln Asn Cys Lys Met 150 Phe Gly Ser Trp Thr Tyr Asp Lys Ala 160 Lys ile Asp Leu Gln Met Glu Arg Thr Val Asp Leu 170
540 AAG GAC TAC TGG GAG AGT GGC GAG 570 TAT AAC AGT AAG AAG TAC GAC TGC TGC GCG GAG ATC TAC
Lys Asp Tyr Trp Glu Ser Gly 180 Trp Ala ile ile Asn Ala Thr Gly Thr 190 Tyr Asn Ser Lys Lys Tyr Asp Cys Ala 200 Glu ile Tyr
630 CCC GAT GTC ACC TAC TAC TTT Tyr Phe 210 660 ATC ATC AAC CTC ATC CCA TGC CTG CTC ATC TCC TGC CTC
Pro Asp Val Thr Tyr Tyr 220 ile Arg Arg Leu Pro Phe Tyr Thr 230 Ser Cys Leu 240
720 ACT GTG CTC GTG TTC TAC CTG CCT 750 TCC GAG TGT GGA GAG AAG ATC ACG CTG TGC Cys 250
Thr Val Leu Val Phe Tyr Leu 260 Ser Glu Cys Gly Glu Lys ile Thr Leu 270
810 CTC ATC ACG GAG ATC ATC CCG TCC 840 ACC TCG CTG GTC ATC CCA CTC ATC GGC 870 ACC CTC TCT
Leu ile Thr Glu ile ile Pro 270 Thr Ser Leu val ile Pro Leu ile Gly 280 Tyr Leu Leu Phe Thr Met ile Phe Val 290 Thr Leu Ser

FIG.15C-2



900 ATC GTT ATC ACA GTC TTC GTG CTC AAT GTA CAC CAC CGC TCC CCC AGC ACC CAC 930 AAC ATG CCC AAC TGG GTA AGS GTA GCC CTG CTA GGC
 Ile Val Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Ser Thr His Asn Met Pro Asn Trp Val Arg Val Ala Leu Gly 960
 300
 990 CGG GTG CCC AGG IGG CTG ATG ATG AAC CGG CCC CTG CCA CCT ATG GAG CTC CAT GGC TCC CCG GAT CTG AAG CTC AGC CCC TCA TAC CAT
 Arg Val Pro Arg Trp Leu Met Met Asn Arg Pro Leu Pro Pro Met Glu Leu His His Glu Ser Pro Asp Leu Lys Leu Ser Pro Ser Tyr His 1050
 330
 1080 TGG CTA GAG ACT AAC ATG GAT GCT GGA GAA AGG GAG ACA GAG GAA GAG GAA GAA GAT GAA AAC ATA TGT GTG TGT GCA GGC
 Trp Leu Glu Thr Asn Met Asp Ala Gly Glu Arg Arg Glu Glu Thr Thr Glu Glu Glu Asp Glu Asn Ile Cys Val Cys Ala Gly 1140
 360
 1170 CTT CCA GAC TCT TCG ATG GGT GTC CTC TAT GGC CAT GGC GGC CTG CAT CTG AGA GCC ATG GAG CCT GAG ACC AAG ACT CCA TCC CAG GCT
 Leu Pro Asp Ser Ser Met Gly Val Leu Tyr Gly His His Gly Glu Glu His Leu Arg Ala Met Glu Pro Glu Thr Lys Thr Pro Ser Gln Ala 1230
 390
 1260 AGC GAG ATT CTG CTG TCA CCT CAA ATA CAG AAA GCA CTA GAA GGT GTA CAC TAC ATT GCT GAC CGT GAT GCT GAC TCT
 Ser Glu Ile Leu Leu Ser Pro Gln Ile Gln Lys Ala Leu Glu Gly Val Val His Tyr Ile Ala Asp Arg Ser Glu Asp Ala Asp Ser 1320
 420
 TCG gtgagt.....ctaacttcag GTG AAG GAA GAC IGG AAG TAT GTG GCC ATG GTG GAC CGG ATA TTC CTC IGG CTG TTC ATT ATC
 Ser Val Lys Glu Asp Trp Lys Lys Tyr Val Val Ala Met Val Val Asp Arg Ile Phe Leu Trp Leu Phe Ile Ile 1380
 450
 1410 GTC TCG TTC CTG GGG ACC ATC GGA CTC TTC CTT CCT CCA TTC CTG GCT GGA ATG ATC TAA CTTTCATGCTCTTCATGTTGGCTCCCAAGGTGGCCTTCGTA
 Val Cys Phe Leu Gly Thr Ile Gly Leu Phe Leu Pro Phe Phe Leu Ala Gly Met Ile 1470
 470
 1500 ACTATCTTCTAGTCTCTGTGATGGAGCCATCTCTAGAAATACTCTTTTGAC.....3'

FIG.15C-3

FIG. 16



FIG.17A

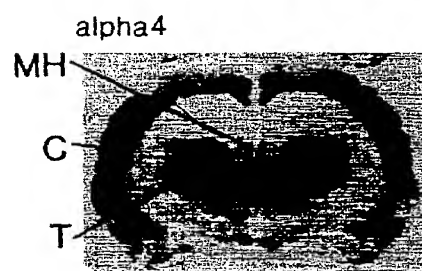
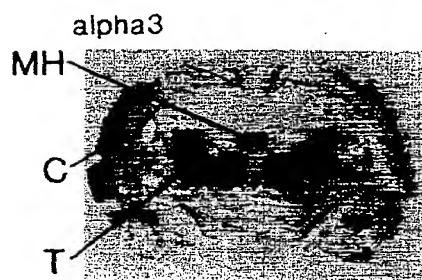
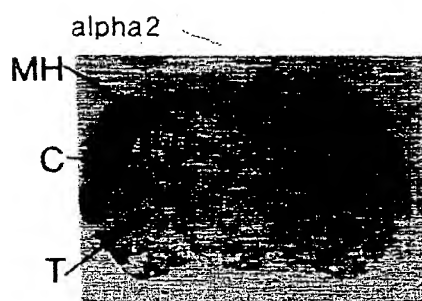
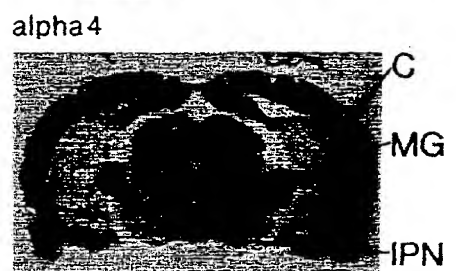
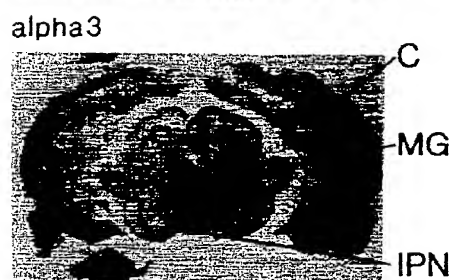
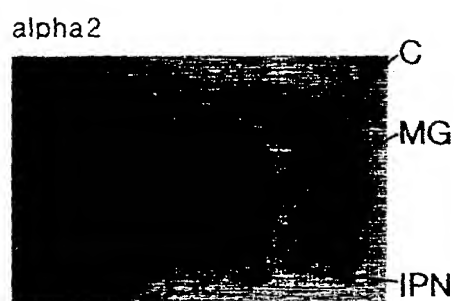


FIG.17B



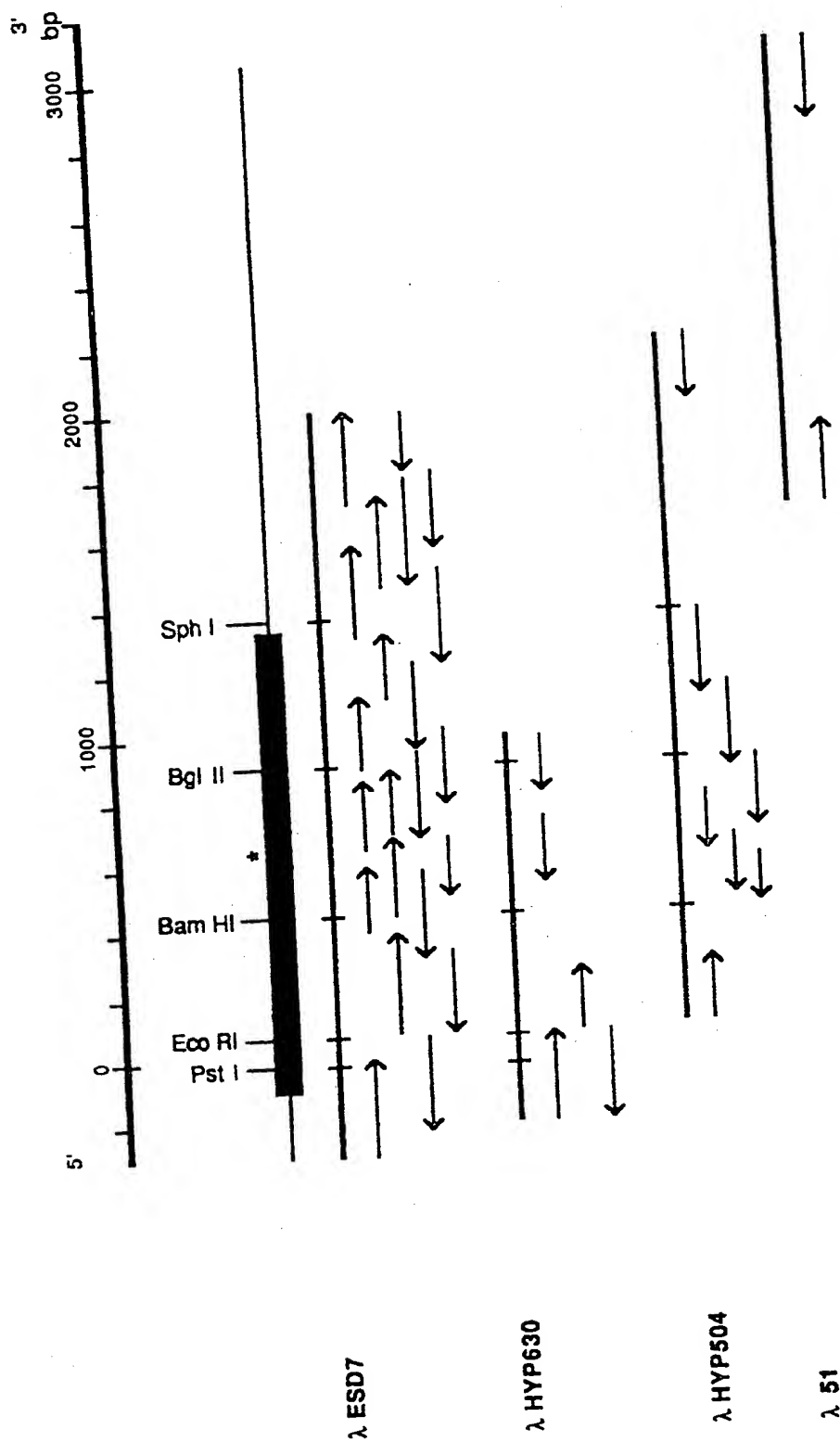
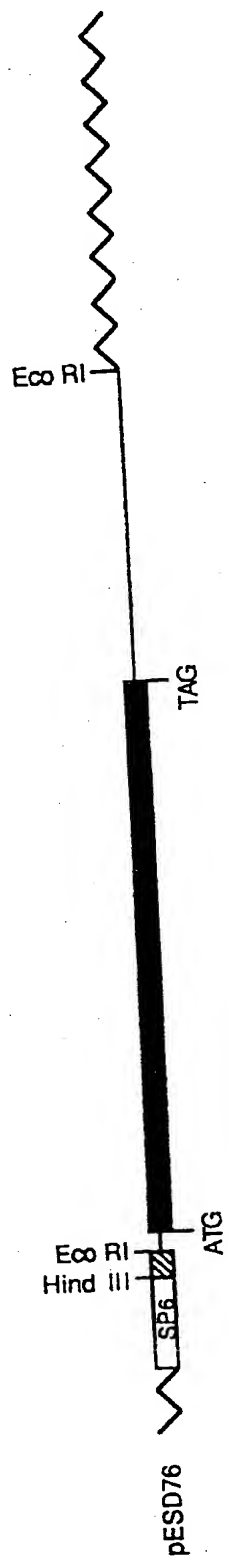


FIG.18A



5'GACAGACATT

-240 -220 -200 -180 -160 -140

TCGCGTCATCAGCTGATATTTTCATCAGGAGCTGGTCACGGCCCTCGGTTTCATCAGGCTTGAACCACTCACAATTTTGTGTTTTTAAACCCCTGATCTCTTCCAGTGGAAACACT

-20 -100 -80 -60 -40

CTGGCCTTGAAGAAATGTCTCTCTGAACCAAGAGTC ATG ACA GGC TTC CTA AGG GTC TTC TTG GTT CTC AGT GCC ACT CTC TCA GGT TCC TGG GTG

-120 -100 -80 -60 -40

Met Thr Gly Phe Leu Arg Val Phe Leu Val Leu Ser Ala Thr Leu Ser Gly Ser Trp Val

-20 -10 10 20 30 40 50

Thr Leu Thr Ala Thr Ala Gly Leu Ser Ser Asp Ile Lys Val Tyr Phe Gly Leu Lys Arg His Leu Phe Gln Gly Tyr Gln Lys Trp Val

-20 -10 10 20 30 40 50

ACT CTT ACG GCC ACT GCA GGA CTC AGC TCA GTG GCT GAA CAC GAA GAC GAA GAC GCA CTC CTC AGA CAT TTG TTC CAA GGT TAC CAG AAA TGG GTC

-20 -10 10 20 30 40 50

Arg Pro Val Leu Asn Ser Ser Asp Ile Lys Val Tyr Phe Gly Leu Lys Ile Ser Gln Leu Val Asp Val Asp Gln Lys Asn Gln Leu

-20 -10 10 20 30 40 50

CGC CCT GTG TTG AAT TCC AGT GAC ATC ATA AAA GTG TAT TTT GGA TTA AAA ATA TCC CAG CTT GTG GAT GTG GAT GAA AAG AAT CAG CTG

-20 -10 10 20 30 40 50

Met Thr Thr Asn Val Trp Leu Lys Gln Glu Trp Thr Asp Gln Lys Leu Arg Trp Asn Pro Gln Glu Tyr Gly Gly Ile Asn Ser Ile Lys

-20 -10 10 20 30 40 50

ATG ACG ACA AAT GTG TGG CTG AAG CAG GAA TGG ACA GAC CAA AAA TTA CGC TGG AAT CCG GAA GAA TAT GGT GGA ATT AAT TCG ATA AAG

-20 -10 10 20 30 40 50

Val Pro Ser Glu Ser Leu Trp Leu Pro Asn Ile Val Leu Phe Glu Asn Ala Asp Gly Arg Phe Glu Gly Ser Leu Met Thr Lys Ala Ile

-20 -10 10 20 30 40 50

GTT CCA TCA GAA TCG CTC TGG CTC CCG GAC ATA GTT CTC TTT GAA AAT GCT GAC GGA CGT TTT GAG GGC TCC CTC ATG ACC AAG GCC ATT

-20 -10 10 20 30 40 50

Val Lys Ser Ser Gly Thr Val Ser Tip Thr Pro Pro Ala Ser Tyr Lys Ser Ser Cys Thr Met Asp Val Thr Phe Phe Pro Phe Asp Arg

-20 -10 10 20 30 40 50

ATG TCC AGT GGA ACC GTC AGC TGG ACT CCT CCC GCC AGC TAC AAG AGT TCC TGC ACC ATG GAT GTC ACA TTT TTC CCG TTC GAC AGG

-20 -10 10 20 30 40 50

340 360 380 400 420

FIG. 19A



150 170
Gln Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Thr Met Val Asp Leu Ile Asn Glu Asn Val Asp Arg Lys Asp
CAG AAC TGC TCG ATG AAG TTT GGA TCC TGG ACT TAC GAC GGT ACC ATG GTT GAC CTC ATC CTA ATC GAA AAC GTT GAC CGG AAA GAC 500

180 200
Phe Phe Asp Asn Gly Glu Trp Glu Ile Leu Asn Ala Lys Gly Met Lys Gly Arg Arg Glu Gly Phe Tyr Ser Tyr Pro Phe Val Thr
TTT TTT GAT AAC AAG GGA GAG TGG GAG ATA CTC AAC GCA AAG GAG GGT AAG GGC TTT TAC TCC TAT CCG TTT GTT ACC 600

210 230
Tyr Ser Phe Val Leu Arg Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Leu Gly Leu Ser Phe Leu Thr Val Leu Val
TAC TCT TTT GTC CTG AGA CGC CTG CCC TTG TTT TAC ACG CTC TTT TTG ATA ATC CCC TGC CTG GGG TTG TCT TTT CTC ACG GTC CTG GTG 680

240 260
Phe Tyr Leu Pro Ser Asp Gly Glu Lys Leu Ser Leu Ser Thr Ser Val Leu Val Ser Leu Thr Val Phe Leu Leu Val Ile Glu Glu
TTC TAC CTA CCC TCG GAC GAA GGG GAA AAA CTC TCA TTA TCC ACC TCC GGT TTG GTC TCT TTG ACG GTG TTT CTT TTA GTG ATT GAA GAA 780

270 290
Ile Ile Pro Ser Ser Lys Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Ile Met Ile Phe Val Thr Leu Ser Ile Ile Val Thr
ATA ATC CCG TCC TCT TCG AAG GTC ATC CCC CTC ATT GGC GAG TAC CTC CTC TTT ATG ATT ATG ATT TTT GTC ACG CTG TCT ATT ATC GTC ACG 860

300 320
Val Phe Val Ile Asn Val His His Arg Ser Ser Ser Thr Tyr His Pro Met Ala Pro Tip Val Lys Arg Leu Phe Leu Gln Arg Leu Pro
GTT TTT GTA ATT AAT GTC CAC CAC CAC AGA TCT TCC TCA ACG TAC CAT CCC ATG GGC CCC TGG GTG AAG AGG CTG TTT CTA CAA AGA CTC CCG 960

330 350
Arg Trp Leu Cys Met Lys Asp Pro Met Asp Arg Phe Ser Phe Pro Asp Gly Lys Glu Ser Asp Thr Ala Val Arg Gly Lys Val Ser Gly
AGA TGG CTT TGC ATG AAG GAC CCC ATG GAC CGC TTC TCT TTC CCG GAT GGA AAG GAG AGT GAT ACA GCC GTG AGG GGG AAA GTC TCA GGC 1040

FIG.19B



Lys Arg Lys Gln Thr Pro Ala Ser Asp Gly Arg Val Leu Val Ala Phe Leu Gln Lys Ala Ser Glu Ser Ile Arg Tyr Ile Ser Arg
AAA AGG AAA CAG ACT CCC GCC AGC GAT GGA GAA AGA GTT CTG CTC GCT TTC CTC GAG AAG GCC TCC GAG TCC ATC AGA TAC ATT TCG AGG
1060 1080 1100 1120 1140 380

His Val Lys Lys Glu His Phe Ile Ser Gln Val Val Gln Asp Trp Lys Phe Val Ala Gln Val Leu Asp Arg Ile Phe Leu Trp Leu Phe
CAT GTG AAA AAG GAA CAC TTC ATC AGC CAG GTA GTG CAA GAC TGG AAA TTT GTG GCT CAA GTT CTG GAC CGC ATC TTC CTG TGG CTC TTT
1160 1180 1200 1220 410

Leu Ile Ala Ser Val Leu Gly Ser Ile Leu Ile Phe Ile Pro Ala Leu Lys Met Trp Ile His Arg Phe His
CTG ATA GCT TCT GTG TTG GGT TCC ATT CTG ATT TTT ATT CCA GCC TTG AAG ATG TGG ATA CAT CAT CGT TTC CAC TAG GAGCCACTCTCTGGACCCA
1240 1260 1280 1300 1320 430

TTTAGAAGACATACATAGAGACMAATCCACCTTAGGACTGACAGCGGCTGGCATCTGACAGGAGCAGCCATCGTAGTGGTCCCTGTCTGTCTGGAGCTTTCTGTG
1340 1360 1380 1400 1420 1440

ATTGAGGGCACTGAGAGMATGTGGTTTGAGTTAGTGTAGTGTGGCTGCCATTAGAGGTGTAGTTGGCAATTTGGAGACGCTCTCCATGTTATATTGTATGTGGGAGTTCTCTGNAAC
1460 1480 1500 1520 1540 1560

TACTCCCTCTGCTCATCCCTGNAAGCAGCTGGGGCTATGTGGTATTCTCTAGCAGCTGTGGTGAACGCAATTTTGACAAATAGTTTCAGGAAATTACCGAGGTACAACTCTCCACACACAGG
1580 1600 1620 1640 1660 1680

TCAATTTCGCCACTTGTCAACGAGTGTCCCAAAATAGGGTCATTGAAGATGACCTTGAATGGCTATGACAGATTCTCTAAGGCAGGTTGTACTGGAAGTTTGTCTCAGCTGACCTGCGNAAC
1700 1720 1740 1760 1780 1800

TTTTCGAATGCAGGTAGGNACTCGGGTGATTTCTAGCTTGTCTGTAAAGTTCCATCAAAATTAAGTTACCCAGAAACAGGCCATTGCGCTAGTAGAACTGTATTTATTTCACACATCTC
1820 1840 1860 1880 1900

TTTTTTTCCC.....3'
1930

FIG.19C

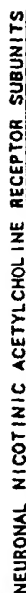
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FIG. 20

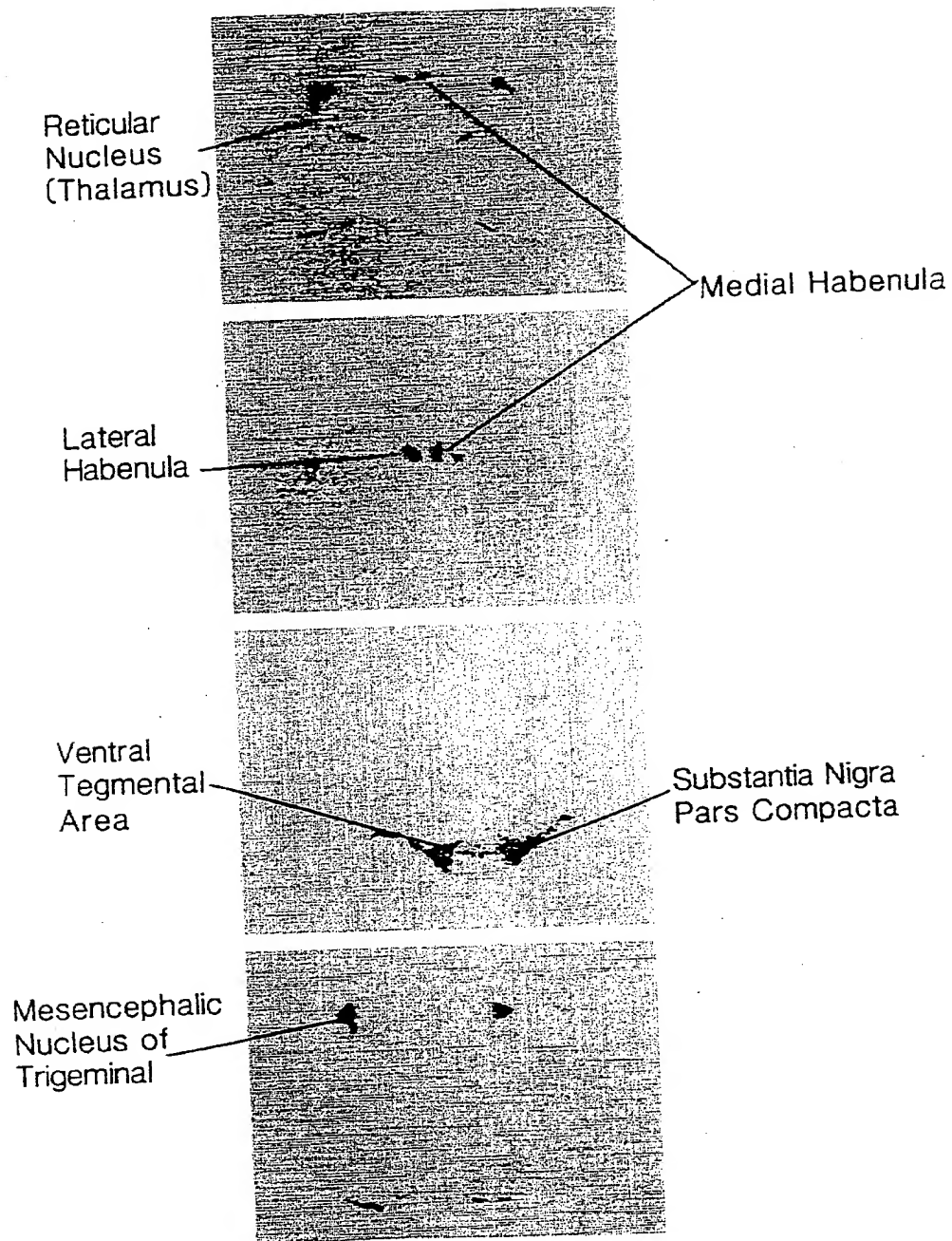


FIG.21



FIG.22

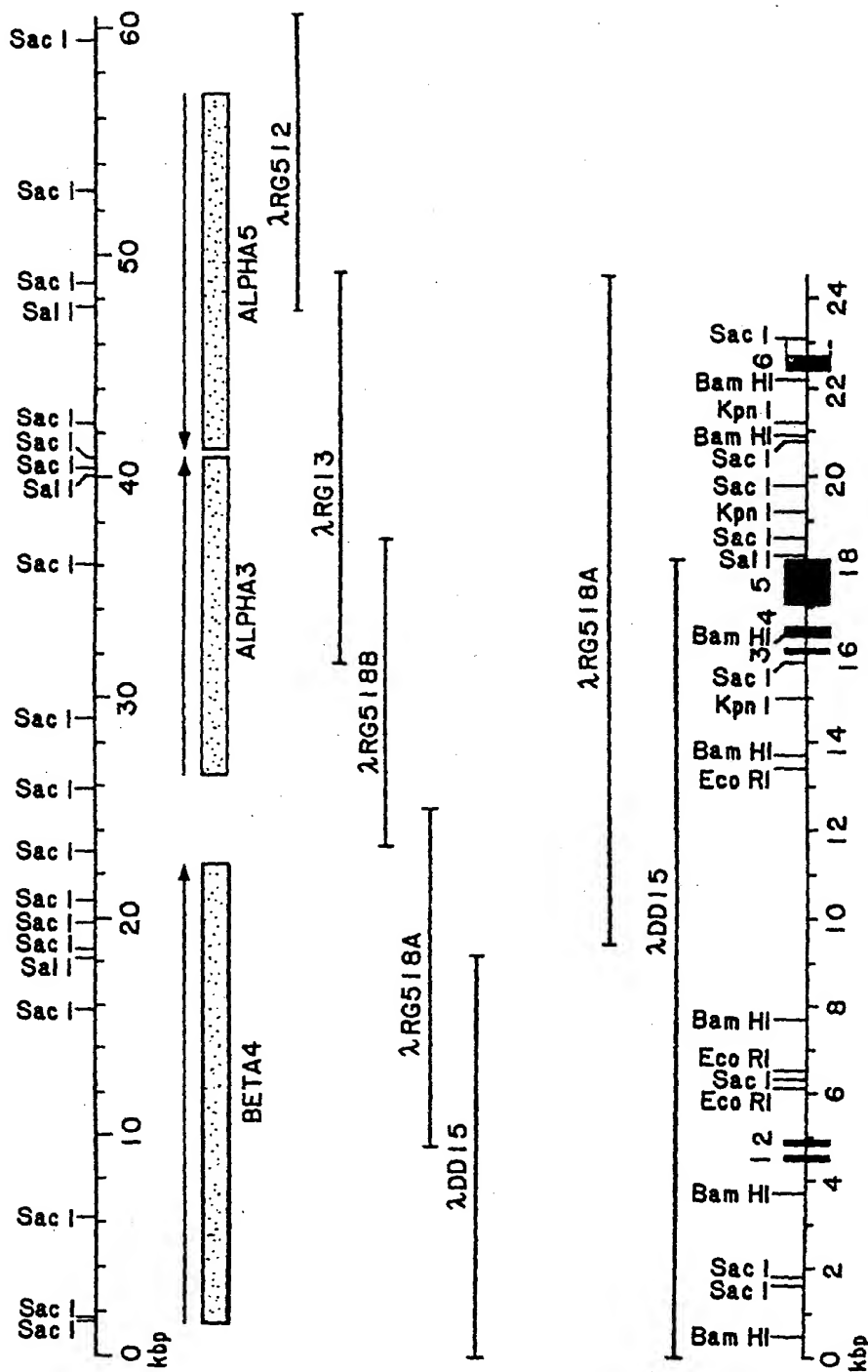
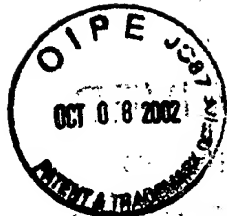


FIG.23



FIG. 24A



130 Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp Gln Gln Asn Cys Thr Leu Lys Phe Arg Ser Trp Thr Tyr
GCT ATC TAC AAG AGT GCC TGC AAG ATT GAG GTG AAG CAC TTT CCC TTC GAC CAG CAG AAC TGC ACC CTC AAA TTC CGC TCC TGG ACC TAT
380 400 420 440 460 480 500 520 540 560 580 600 620 640 660 680 700 720 740 760 780 800 820 840 860 880 900 920 940 960 980 1000

160 Asp His Thr Glu Ile Asp Met Val Leu Lys Ser Ala Thr Ala Ile Met Asp Phe Thr Pro Ser Gly Glu Trp Asp Ile Val Ala Leu
GAC CAC ACG GAG ATT GAC ATG GTT CTT AAG TCG CCC ACG GCC ATC ATG GAT GAC TTC ACC CCC AGT GGT GAA TGG GAC ATT GTG GCC CTC
480 500 520 540 560 580 600 620 640 660 680 700 720 740 760 780 800 820 840 860 880 900 920 940 960 980 1000

190 Pro Gly Arg Arg Thr Val Asn Pro Gln Asp Pro Ser Tyr Val Asp Val Thr Tyr Asp Phe Ile Ile Lys Arg Lys Pro Leu Phe Tyr Thr
CCA GGA CGG AGG ACG GAG AAC CCT CAG GAC CCC AGC TAC GTG GAC GTG ACC TAT GAC TTC ATC ATC AAG CGC AAC GCG CTC TTC TAC ACC
560 580 600 620 640 660 680 700 720 740 760 780 800 820 840 860 880 900 920 940 960 980 1000

220 Ile Asn Leu Ile Ile Pro Cys Val Leu Ile Thr Ser Leu Ala Ile Leu Val Phe Tyr Leu Pro Ser Asp Cys Gly Glu Lys Met Thr Leu
ATC AAT CTT ATC ATT CCT TGT GTG CTC ATC ACC TCG CTG GCT ATC CTG GTC TTC TAC CTG CCC TCC GAC TGT GGG GAG AAG ATG ACG CTC
660 680 700 720 740 760 780 800 820 840 860 880 900 920 940 960 980 1000

250 Cys Ile Ser Val Leu Leu Ala Leu Thr Phe Phe Leu Leu Ile Ser Lys Ile Val Pro Pro Thr Ser Leu Asp Ile Pro Leu Ile Gly
TGC ATC TCT GTG CTG GCA CTC ACG TTC TTC CTG CTG CTC ATC TCC AAG ATC GTC CCG CTT GAC ATA CCG CTC ATT GGC
740 760 780 800 820 840 860 880 900 920 940 960 980 1000

280 Lys Tyr Leu Leu Phe Thr Met Val Leu Val Thr Phe Ser Ile Val Thr Thr Thr Val Cys Val Leu Asn Val His His Arg Ser Pro Ser Thr
AAG TAC CTC TTG TTC ACC ATG GTG CTC GTC ACC TTT TCC ATC GTC ACC ACT GTG TGT GTC CTC AAT GTG CAC CAC CGC TCA CCC AGC ACT
840 860 880 900 920 940 960 980 1000

310 His Thr Met Ala Ser Trp Val Lys Glu Cys Phe Leu His Lys Leu Pro Thr Phe Leu Phe Met Lys Arg Pro Gly Leu Ser Leu
CAC ACC ATG GCA TCC TGG GTC AAG GAG TGC TTC CTG CAC AAA CTG CCC ACC TTC CTC TTC ATG AAG CGT CCC GGT CTT GAA GTC AGC CTG
920 940 960 980 1000

FIG.24B

Val Arg Val Pro His Pro Ser Gln Leu His Leu Ala Thr Ala Asp Thr Ala Ala Thr Ser Ala Leu Gly Pro Thr Ser Pro Ser Asn Leu	340	350	360
5TC AGG GTC CCT CAT CCC AGC CAG CTG CAC TTG GCC ACA GCT GAT ACT GCA GCC ACC TCT GCC TTA GGC CCC ACC GCA TCC AAC CTC	1020	1040	1080
370	1100	1120	1140
Tyr Gly Ser Ser Met Tyr Phe Val Asn Pro Val Pro Ala Ala Pro Lys Ser Ala Val Ser Ser His Thr Ala Gly Leu Pro Arg Asp Ala			
TAT GGG AGT TCC ATG TAC TTT GTG AAC CCT GTC CCT GCC GCT CCT AAG TCT GCA GTC AGC TCC CAC ACA GCA GGC CTC CCC AGG GAT GCC	1100	1120	1160
380	1180	1200	1220
Arg Leu Arg Ser Ser Gly Arg Phe Arg Glu Asp Leu Gln Glu Ala Leu Gln Gly Val Ser Phe Ile Ala Gln His Leu Glu Ser Asp Asp			
CGT CTG AGG TCC TCC GGG AGG TTC CGG GAA GAT CTA CAG GAA GCA TTA GAG GGT GTC AGC TTC ATC GCC CAG CAT CTG GAG AGC GAT GAC	1200	1220	1260
400	1280	1300	1320
Arg Asp Gln Ser CGA GAT CAA AGT gtatcactg...			
Val Ile Glu Asp Trp Lys Phe Val Ala Met Val Val Asp Arg Arg Leu Phe Leu Trp	430	440	450
...ttgtctgcag GTC ATC GAG GAC TGG AAG TTC GTC GCG ATG GTT GTT GAC CGC CTG TTC CTG TGG	1280	1300	1320
460	1340	1360	1380
Val Phe Val Phe Val Cys Ile Leu Gly Thr Met Gly Leu Phe Leu Pro Pro Leu Phe Gln Ile His Ala Pro Ser Lys Asp Ser			
GTG TTC GTG TTT GTG TGT ATT CTG GGC ACC ATG GGG CTC TTC CTC CCA CCC CTT TTC CAG ATC CAC GCA CCC TCC AAG GAC TCC TAG GCT	1340	1360	1400
470	1420	1440	1460
ACCCGGCNTGTCTCGGNNCCGGGAAGCTAGTGAATGATATGAGAGCGGTGGGAAGCAGGGCGTGTCTTNGGCTACCCGGCTGTCTCGGCCCCGGGAAGTAGTGAGATGATGATGA	1420	1440	1480
1500	1520	1540	1560
GAAACGGGTGGGAAGCAGGGCGTGTCTTCGG...3'			
1540	1560	1580	1600

FIG. 24C



Phe	Leu	Ile	Ile	Pro	Cys	Ile	Gly	Ile	640	Leu	Pro	Asn	Glu	Gly	Glu	Lys	Ile	Ser	Leu	Cys	240	
TTT	CTT	ATT	ATC	CCC	TGC	ATT	GGG	660	Leu	Ser	TCA	ACC	GAG	GGT	GAA	AAG	ATT	AGC	CTC	TGC	720	
Leu	Ser	Phe	Leu	Thr	Val	Val	GTT	680	Leu	Pro	CCT	TCA	AAC	GAG	GAG	GAA	AAG	ATT	Ser	Leu	240	
CTC	TCA	TTT	CTG	ACT	GTT	GTT	GTC	680	CTC	CTC	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT	720	
Thr	Ser	Val	Leu	Val	Ser	Leu	Thr	740	Pro	Ser	Ser	Ser	Lys	Val	Ile	Pro	Leu	Ile	Gly	Glu	270	
ACC	TCA	GTG	CTC	GTG	TCT	CTG	ACT	740	CCA	TCA	TCT	TCC	AAA	GTC	ATA	CCC	CTG	ATT	GGG	GAG	720	
Ile	Leu	Val	Phe	Thr	Met	Ile	Phe	800	Ala	Ile	Asn	Ile	His	His	Arg	Ser	Ser	Ser	Thr	His	300	
TAC	TTG	GTG	TTT	ACC	ATG	ATT	TTT	800	GCC	ATC	AAC	ATC	CAC	CAC	CGC	TCT	TCC	TCC	ACA	CAC	900	
Leu	Val	Val	Thr	Leu	Ser	Ile	Met	860	Val	Thr	Val	Val	Thr	Val	Thr	Val	Thr	Val	Thr	Val	300	
CTG	GTG	GTG	ACT	CTA	TCC	ATT	ATG	860	GTG	ACC	CTA	TCC	ACT	GTG	ACT	GTG	ACT	GTG	ACT	GTG	900	
Asn	Ala	Met	Ala	Pro	Trp	Val	Arg	920	Lys	Ile	Phe	Leu	His	Lys	Leu	Pro	Cys	Arg	Arg	Thr	330	
AAC	GCT	ATG	GCG	CCC	TGG	GTT	CGT	920	AAG	ATA	TTT	CTC	CAC	AAG	CTT	CCC	AAG	TAC	TAC	ACT	330	
Gln	Arg	Glu	Glu	Ala	Glu	Ser	Gly	1000	Arg	Gly	Pro	Lys	Ser	Arg	Asn	Thr	Leu	Ile	Thr	Arg	360	
CAG	AGA	GAA	GAA	GAA	GCC	GAG	AGT	1000	GCT	GGG	CCT	AAA	TCT	CGG	AAC	ACT	TTG	ATC	ATC	AGG	360	
Leu	Val	Lys	Glu	Asn	Asp	Val	Arg	1100	Glu	Val	Val	Glu	Asp	Arg	Met	Phe	Leu	Trp	Thr	Phe	390	
GTG	GTG	AAA	GAG	AAC	GAC	GTG	CGC	1100	GTT	GTT	GTT	AAA	TTT	ATA	GCC	CAA	GTC	ATG	TTT	CTT	390	
Leu	Val	Ser	Ile	Ile	Gly	Thr	Leu	1180	Gly	Leu	Phe	Val	Ile	Ile	Val	Pro	Val	His	Ile	Asn	Thr	420
CTG	GTG	TCA	ATC	ATT	GGG	ACT	TTA	1180	GGG	CTT	TTT	GTT	CTT	CTT	ATA	ATA	GTC	CCA	GTT	CAC	420	
Val	Val	Ser	Ile	Ile	Gly	Thr	Leu	1200	Gly	Leu	Phe	Val	Ile	Ile	Val	Pro	Val	His	Ile	Asn	Thr	420
CTG	GTG	TCA	ATC	ATT	GGG	ACT	TTA	1200	GGG	CTT	TTT	GTT	CTT	CTT	ATA	ATA	GTC	CCA	GTT	CAC	420	

FIG. 25B



Ile Lys •
ATT AAG TGA AACCAAGAAATTACCCTGTGGATTAGTGAGCAGTCATGCAGCTCTTAGGACATGTATGCTGTTATGGAATGTGAAGGTAGTTACAATTTGACATAGGCTATAACA 1380
1320
GATTAGCAATTTCTAACATTGGCTTAATGTGTCATAGAACTGCAGTAATAAACCCTCAATAGCAACAACACACATTGTCTGCCTGCACCTAGTAGAAGGCCCTAGCATCTGCATCCTGGGCAA 1500
1420
ACCCTACCAATTTGCAACCAATGATGAAGGCCATCCTTGGAGTGCTGGAAACTCAACTGTATTGGAAGACTATTAAACTCCCCCAAAATTTAGTGAAGAACATATATATGTGTGGTT 1620
1520
TTGAATTTTCAGAAATGGGCTTTGGGCTTTGTTAAATTTGCTGGGCTAGCACAAACCTCCTGAGTAGCTGGGACCATGGGTGTGCTCCACTTTGCCCTGTCTGTATTCACAGATATA 1720
1640
AAATACATCATTTATTTATAGGAGGTAGGCCCATTTACTTTGGTTTAATAATAACTTAATGTAGGTTTAGGTTAATTAATATTAACCTTATGTCAAGCTAATGTCTATTGCTGTGAAGAGACATC 1840
1760
ATGACCATCAACTCTTATAAAGAAACATTTTCATCAGTGCTGGCTTACAGTTTTTGAGGTTTAGCCCAATTATCACAGTGGAAGCATGATAGCATCCAGGTAGACATATAATGCTGGATCC 1960
1880
AGGAGTTCTCTACATCTGGATCAGCAGGCAGGAAAGAGAGAGAGGCCACTGGACCTGGCTTGAGCATCTGAACCTCAAGCCCCACCCTCCAGTGACACACTTCCCCCAACAAGGCC 2080
2000
ACACCTCCTAATAGTGCCACTTGGTGATCAAGCATTTCACTCTTTATATGGAATATGGATTGGCTTTTATTAATACTTCAACACCACACTTAATAGGATGCTATTCTTTACTGACATTTTAAATAAG 2200
2120
CGACAAATGGTAAC TAGAACAATCGTAGGCCCACTTTACTCTTTTATATGGAATATGGATTGGCTTTTATTAATACTAGTTTTTACAGCCCTATCTGAACACATGTAAACAGGCAACTCCTG 2320
2240
CAGACACATTTCTTTGTAATGACTTTTATAATCCTGCAGTGCCATGTTCTGCTGATGACTCTCCTCGCCACACTCCTCCGGTTAGTAGGCCATTTATGTACATCGCGTATCCCTG 2440
2360
ATTTCAGAGCAACTGTGCAGTTGCACAGGTTCCACCTCAAAATGGGATGCCATGACTGTCTGCTGGATAATTCTGTGGAAAAACCACTTCTGAGCTGGATACGGTGCCTCATACCTGTCA 2560
2480
TGCTACTTTTCAGGAGGCAGAGGGGAAATTGCTGTGAGTTGTTGGTCAGCCTGGGTTACATATGAGACCCCTGTCTCAGAAACCCAAACAAACTTCCCCCTGTGAGTTGATATAAG 2680
2580
CACACTGTCATATCCGAATTTGGGGATCCTCTAGAGTCGACCTGCAGGCCATGCAAGCTTGGCTCATAGCTGTTTCCCTGTGTGAATTTGTTATCCG 2780
2700

FIG.25C



BETA2 MLCMAGHNSMALFS SLLMLCSGVLGTDTEERLVEHLDDPSRYNKLIRPATNGSELVTVOLMVSLAQLSVHEREQIMTTNVWLTOEWEDYRLTWKPEDFDNMK
BETA3 MTGFLRVFLVLSATLSGSWVLTATAGLSSVAEHEDALLRHLFGQYQKWPVPVLSNDIIKVFYGLKISQLVDVEKNQIMTTNVWLKQEWTDQKLRWNPPEEYGGIN
BETA4 MRGTPLLVLSLFSLLQDQDCRLANAEKMDLLNKNTRYNNLIRPATSSQLISIRLELSQLISVNEREQIMTTISWLKQEWTDYRLAMNSSCYEGVN
----- SIGNAL PEPTIDE -----

BETA2 KVRLP SKHIWLPDVVLYNNADGMYEVSFYSHNAVSYDGSIFWLPPIAYKSAKIEVKHFPFQQNCTMKFRSWTYDRTEIDLVLKSDVASLODFTPSGENDIIALPG
BETA3 SIKVPSSESLWLPDIVLFENADGRFEGSLMTRKAIKSSGTVSWTPPASYSKSSCTMDVTFPPDRQNCMSKFGSWTYDGTMDVLILINENVDRKDFDNGEWEILNARG
BETA4 ILRIPAKRVWLPDIVLYNNADGMYEVSFYSHNAVSYDGSIQWLPPIAYKSAKIEVKHFPFQQNCTMKFRSWTYDRTEIDLVLKSDVASLODFTPSGENDIIALPG

BETA2 RRNENPDOS TYVDITYDFIIRKKPLFYTTINLIIPCVLITSLAILVFLPSPDCGERMTLCISVLLALTVELLLISKIVPPTSLDVLVGVKYLMTMVLVTFISVTSV
BETA3 MKGHRREGYSYFFVTYSFVLRRLPLFYTTLELIIPCGLSFLTVLVFLPSPDCGERMTLCISVLLALTVELLLISKIVPPTSLDVLVGVKYLMTMVLVTFISVTSV
BETA4 RRTVNPQDP SYVDVTYDFIIRKKPLFYTTINLIIPCVLITSLAILVFLPSPDCGERMTLCISVLLALTVELLLISKIVPPTSLDVLVGVKYLMTMVLVTFISVTSV
----- MSR I ----- MSR II ----- MSR III -----

BETA2 CVLNVVHRRSPTT HTMAPWVKVVFLEKLPITLFLQPRHRCARQRLRRRQREGEAVFFREGPAADPCSVGPCSCG
BETA3 FVINVHRRSSSTYHMAPWVKRLFLQRLPRWLCMKDPNDRFSFPDGKESDTAVRGVSGKRKOTPASDGERVLVAFLEK
BETA4 CVLNVHRRSPST HTMASWVKECFLHKLPTFLFNKRPGLEVSLVRVPHPSQLHATADTAATSALGPTSFNSLYGSSMYFVNPVPAAPKSAVSSHTAGLPRDARLRS

BETA2 LREAVDGVRFIADHMRSEDDDDQSVREDWKYVAMVIDRLFLWIFVFCVGTGMLQPLFQNYTATTFLHPDHSAPSSK*
BETA3 ASESIYISRHVKKEHFISQVQDNKFXVAQVLDRLFLWFLIASVLGSLILIFIPALAMNHRFH*
BETA4 SGRFREDLQALEGVSFIAQHLESDDRDQSVIEDWKYVAMVVDRLFLWVFCVILGTMLGLFLFPLFQIHAPSND*
----- MSR IV -----

FIG.26



ALPHA2 MTLSHSALQFMTLHLMCLLLVPAVLTQOQSHTHAEDRLFXHLFGGYNRWARPVNTSDVIVREFGLSIAQLIDVDENQOMMTTNVWLKQEWNDYKLRNDPAE
ALPHA3 MGVLPLPPLSMLMLVLMPLPAASASEAHERLFQYLFEDYNEIIRPVANVSHPIIQFEVMSQLVKVDEVNQIMETNMLKQWMDYKLRWKPSD
ALPHA4 MEIGGPGAPPPILLPLLLGLTGLLPASSHETRAHAERLLKRLFGYGNKMSRPVGNISDVULVREFGLSIAQLIDVDENQOMMTTNVWLKQEWNDYKLRNDPDD
ALPHA5 MVQLLAGRWRTGARRGTAGGLBELSSAAKHEDSLFRDLFEDYERWVRVVEHLSDKIKIFGLAISQLVDVDENQOMMTTNVWLKQEWNDYKLRNDPDD

SIGNAL PEPTIDE

ALPHA2 FGNVTSRVPSEMIWIPDIVLNNADGEFAVTHMKAHLFFTGTVHWPVPAIYKSSCIDVTFPPDQONCKMFGSWTYDKAKIDLQOMERTVDLKDYMESGEWA
ALPHA3 YQGVFHRVPAEKINWKPDIVLNNADGDFQVDDKTRAILKXYTGVTWIPPAIFKSSCKIDVTFPPDQONCKMFGSWTYDKAKIDLQOMERTVDLKDYMESGEWA
ALPHA4 YENVTSIRIPSELIWIPDIVLNNADGDFAVTHLTKARLFYDGRVQMTWIPPAIYKSSCIDVTFPPDQONCKMFGSWTYDKAKIDLQOMERTVDLKDYMESGEWA
ALPHA5 YGGIKIIRVPSDSLWIPDIVLNNADGREGAS TKTVRYNGTGTWTPANYKSSCTIDVTFPPDQONCKMFGSWTYDKAKIDLQOMERTVDLKDYMESGEWA

ALPHA2 IINATGYNSKKYDCCAEIYDPVTYFVIRBLPLFYINLIIPCLLISCLTVLVFYLPSCEGKITCLISVLLSLTVFLLLTETIIPSTSLVPLIGEXYLLFTMIF
ALPHA3 IINATGYNSKKYDCCAEIYDPVTYFVIRBLPLFYINLIIPCLLISCLTVLVFYLPSCEGKITCLISVLLSLTVFLLLTETIIPSTSLVPLIGEXYLLFTMIF
ALPHA4 IVDVAVGYNTRKYDCCAEIYDPVTYFVIRBLPLFYINLIIPCLLISCLTVLVFYLPSCEGKITCLISVLLSLTVFLLLTETIIPSTSLVPLIGEXYLLFTMIF
ALPHA5 IINATGYNSKKYDCCAEIYDPVTYFVIRBLPLFYINLIIPCLLISCLTVLVFYLPSCEGKITCLISVLLSLTVFLLLTETIIPSTSLVPLIGEXYLLFTMIF

MSR I MSR II MSR III

ALPHA2 VTLISIVITVFLNVHHRSPSTHNMFN MVRVALLGRVPRWLMNMRPLPPMELHSGSPDLKLPSPYHMLETNMDAGERETETEREEEDENICVCAGLPDSSMGVLYG
ALPHA3 VTLISIVITVFLNVHHRSPSTHNMFN MVRVALLGRVPRWLMNMRPLPPMELHSGSPDLKLPSPYHMLETNMDAGERETETEREEEDENICVCAGLPDSSMGVLYG
ALPHA4 VTLISIVITVFLNVHHRSPSTHNMFN MVRVALLGRVPRWLMNMRPLPPMELHSGSPDLKLPSPYHMLETNMDAGERETETEREEEDENICVCAGLPDSSMGVLYG
ALPHA5 VTLISIVITVFLNVHHRSPSTHNMFN MVRVALLGRVPRWLMNMRPLPPMELHSGSPDLKLPSPYHMLETNMDAGERETETEREEEDENICVCAGLPDSSMGVLYG

ALPHA2 HGLHLRAMEPETKTPSQA
ALPHA3 THSSSSSESVNAV
ALPHA4 TCRSPPLEVPDLXTSEVENKASPCPSGCPKSSSGAPMLIKARSLSVQHVPSSQEAEDGIRCRSRSIQCVSQDGAASLADSNKPTSPSTSLKARPSQLPVSDQ
ALPHA5

ALPHA2 SEILLSPQIQKALEGVHYIADIRSEADSSVKEDWKYVAMVVDRIFLWLFIIVCFGLGTIGLFPFLAGMI*
ALPHA3 SLSALSPEIKAEIQSVKYIAENKKAONVAKEIQDDWKYVAMVIDRIFLWLFIIVCFGLGTIGLFPFLAGMI*
ALPHA4 ASPCKCTCKEPPSPVTVLKAGGTAKPPQHLPLSPALTRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLWLFIIVCFGLGTIGLFPFLAGMI*
ALPHA5 LEAALDCIRYITRHHVVKENDREVVEDWKFLAQVLDRMFLWTFLLVSIIGTLGLFVPVFFINGPI*

MSR IV

FIG.27

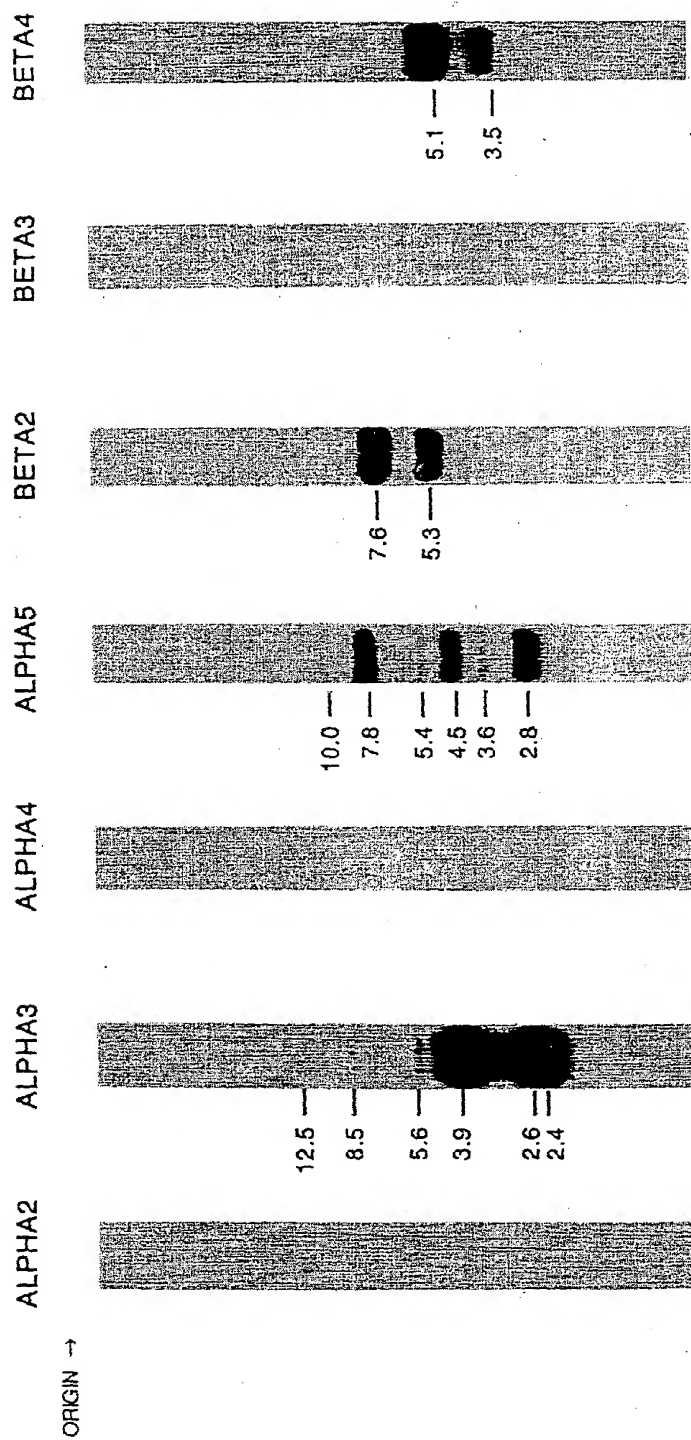


FIG.28

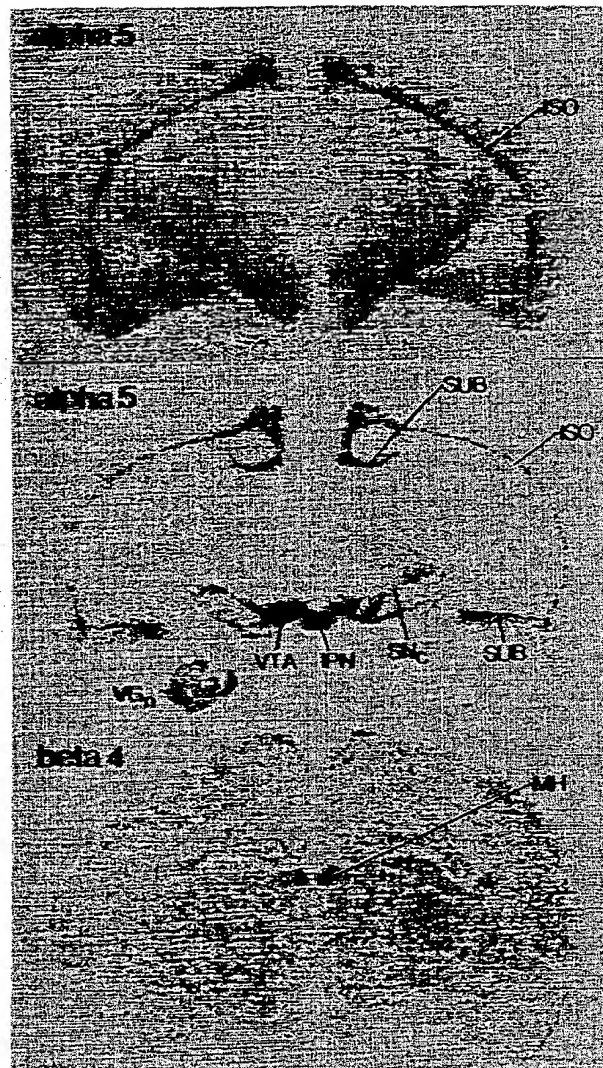


FIG.29